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PATENT APPLICATION

TAG NUCLEIC ACIDS AND PROBE ARRAYS

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TAG NUCLEIC ACIDS AND PROBE ARRAYS

PRIORITY CLAIM

This application claims priority of U.S. Provisional Application 60/195,585 filed April 6, 2000 entitled "Tag Nucleic Acids and Probe Arrays", which is incorporated herein by reference for all purposes in its entirety.

FIELD OF THE INVENTION

This invention provides sets of nucleic acid tags, arrays of oligonucleotide probes, nucleic acid-tagged sets of recombinant cells and other compositions. The invention relates to the selection and interaction of nucleic acids, and nucleic acids immobilized to solid substrates, including related chemistry, biology, and medical diagnostic uses.

BACKGROUND OF THE INVENTION

The use of short nucleic acid sequences as "tags" to identify specific biological substances in a sample is known. For example, tags may be used as a method of or as labels for a wide variety of biological and nonbiological materials, see, for example, Dollinger, The Polymerase Chain Reaction pp. 265-274 Mullis et al., editors (Birkhauser, Boston, 1994) or as a method of screening complex chemical libraries. See, for example, Alper, Science, 264: 1399-1401 (1994); and Needels et al. PNAS 90, 10700-10704 (1993). See also US Patent Nos. 4,359,353, 4,441,943, 5,451,505 and 5,654,413.

There is great necessity for sets of tag sequences which are known to hybridize effectively to their complementary probe sequences with minimal cross-hybridization between the different tag sequences. The presently claimed invention provides sets of tag sequences, tag sequence kits, and methods of using tag sequences which fulfill these requirements.

SUMMARY OF THE INVENTION

The presently claimed invention provides 2050 unique sequences which have been specifically chosen according to strict criteria to produce sequences suitable for a wide variety of “tagging” applications. These sequences are provided as SEQ ID NOs 1-2050.

In one embodiment, some or all of SEQ ID Nos 1-2050 comprise tag sequences. In a further embodiment, some or all of SEQ ID Nos 1-2050 comprise tag-probe sequences. In a further embodiment, the tag-probe sequences are immobilized to a solid support.

The unique sequences of the presently claimed invention may be used alone or in combinations of 10 or more, 100 or more, 200 or more, 500 or more, 1000 or more, 1500 or more, or 2000 or more as nucleic acid tags and/or tag-probes.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 shows a plot of the discrimination score and the signal intensity for 2200 candidate sequences.

FIG. 2 shows an example of the sequences attached to each of the four array features representing a given tag sequence. Four features, organized vertically on the probe array, represent each tag-probe.

FIG. 3 shows the array features from an array designed to probe for the tag sequences of the presently claimed invention. For each of the four tag-probes shown, arranged horizontally across the array, the brightest hybridization signal is seen with the “PM” feature.

FIG. 4 is a scanned image of the hybridization patterns resulting from the hybridization of 2050 different probes containing regions complementary to the SEQ ID Nos 1-2050 to an array comprised of tag-probes corresponding to SEQ ID Nos 1-2050.

FIG. 5 is a scanned image of the hybridization patterns resulting from the hybridization of 50 different probes containing regions complementary to SEQ ID Nos 2001-2050 to an array identical to the array depicted in FIG. 4.

FIG. 6 shows signal intensities from two different independent experiments in which 2000 biotinylated oligonucleotide tags or 50 fluorescein labeled control oligonucleotides were hybridized to arrays designed as described above.

FIG. 7 shows the PM/MM ratios from the data described in FIG. 4 above.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

I. Definitions

As used herein, certain terms may have the following defined meanings.

As used in the specification and claims, the singular forms “a”, “an” and “the” include plural references unless the context clearly dictates otherwise. For example, the term “an array” may include a plurality of arrays unless the context clearly dictates otherwise.

An “array” represents an intentionally created collection of molecules which can be prepared either synthetically or biosynthetically. In particular, the term “array” herein means an intentionally created collection of polynucleotides attached to at least a first surface of at least one solid support wherein the identity of each polynucleotide at a given predefined region is known. The terms “array,” “biological chip” and “chip” are used interchangeably.

The array of molecules can be screened for biological activity in a variety of different formats (*e.g.*, libraries of soluble molecules, libraries of compounds tethered to resin beads, fibers, silica chips, or other solid supports). The fabrication of polynucleotide arrays on a solid substrate, and methods of use of the arrays in different assays, are described in US Patent Numbers: 5,143,854, 5,242,979, 5,252,743, 5,324,663, 5,384,261, 5,405,783, 5,412,087, 5,424,186, 5,445,934, 5,451,683, 5,482,867, 5,489,678, 5,491,074, 5,510,270, 5,527,681, 5,550,215, 5,571,639, 5,593,839, 5,599,695, 5,624,711, 5,631,734, 5,677,195, 5,744,101, 5,744,305, 5,744,992, 5,753,788, 5,770,456, 5,831,070, 5,856,011, 6,040,138 and 6,040,193 all of which are incorporated by reference herein in their entireties for all purposes. See also, US Serial Nos. 09/079,324, 09/122,216, and PCT Application WO US99/00730 each of which is incorporated by reference herein in its entirety for all purposes. Preferred arrays contemplated by the presently claimed invention have the probe densities as described in the above referenced patents. For example, the ‘305 patent discloses 100, 400, 1,000 and 10,000 probes/cm².

"Solid support," "support," and "substrate" refer to a material or group of materials having a rigid or semi-rigid surface or surfaces. In many embodiments, at least one surface of the solid support will be substantially flat, although in some embodiments it may be desirable to physically separate synthesis regions for different compounds with, for example, wells, raised regions, pins, etched trenches, or the like. According to other embodiments, the solid support(s) will take the form of beads, resins, gels, microspheres, fibers or other geometric configurations.

A "discrete, known location" refers to a localized area on a solid support which is, was, or is intended to be used for placement or fabrication of a selected molecule and is otherwise referred to herein in the alternative as a "selected" region. The discrete, known location may have any convenient shape, *e.g.*, circular, rectangular, elliptical, wedge-shaped, etc. For the sake of brevity herein, "discrete, known locations" are sometimes referred to as "predefined regions," "regions," or "features." In some embodiments, a discrete, known location and, therefore, the area upon which each distinct compound is synthesized is smaller than about 1 cm² or even less than 1 mm². In additional embodiments, a discrete, known location can be achieved by physically separating the regions (*i.e.*, beads, fibers, resins, gels, etc.) into wells, trays, etc.

As used herein, a "polynucleotide" is a sequence of two or more nucleotides. Polynucleotides of the present invention include sequences of deoxyribonucleic acid (DNA) or ribonucleic acid (RNA) which may be isolated from natural sources, recombinantly produced, or artificially synthesized. A further example of a polynucleotide of the present invention may be polyamide polynucleotide or peptide nucleic acid (PNA). This invention also encompasses situations in which there is nontraditional base pairing such as Hoogsteen base pairing which has been identified in certain tRNA molecules and postulated to exist in a triple helix. "Polynucleotide" is used interchangeably with "oligonucleotide" in this application.

The terms "nucleotide" and "nucleic acid base" include deoxynucleotides and analogs thereof. These analogs are those molecules having some structural features in common with a naturally occurring nucleotide such that when incorporated into a polynucleotide sequence, they allow hybridization with a complementary polynucleotide in solution. Typically, these analogs may have one or more modified bases, as well as modified forms of ribose and phosphodiester moieties. The changes can be tailor made to stabilize or destabilize hybrid formation, enhance

the specificity of hybridization with a complementary polynucleotide sequence as desired, or enhance stability of the polynucleotide.

The terms "nucleic acid," "nucleic acid molecule," or "nucleic acid sequence," refer to a deoxyribonucleotide or ribonucleotide polymer in either single-or double-stranded form, and unless otherwise limited, would encompass analogs of natural nucleotides that can function in a similar manner as naturally occurring nucleotides. Nucleic acids may be derived from a variety of sources including, but not limited to, naturally occurring nucleic acids, clones, synthesis in solution or solid phase synthesis.

As used herein a "probe" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (*i.e.* A, G, U, C, or T) or modified bases (7-deazaguanosine, inosine, *etc.*). In addition, the bases in probes may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.

The term "target nucleic acid" or "target sequence" refers to a nucleic acid or nucleic acid sequence which is to be analyzed. A target can be a nucleic acid to which a probe will hybridize. The probe may or may not be specifically designed to hybridize to the target. It is either the presence or absence of the target nucleic acid that is to be detected, or the amount of the target nucleic acid that is to be quantified. The term target nucleic acid may refer to the specific subsequence of a larger nucleic acid to which the probe is directed or to the overall sequence (*e.g.*, gene or mRNA) whose expression level it is desired to detect. The difference in usage will be apparent from context.

The term "hybridization" refers to the process in which two single-stranded polynucleotides bind non-covalently to form a stable double-stranded polynucleotide; triple-stranded hybridization is also theoretically possible. The resulting (usually) double-stranded polynucleotide is a "hybrid." The proportion of the population of polynucleotides that forms stable hybrids is referred to herein as the "degree of hybridization." Hybrids can contain two DNA strands, two RNA strands, or one DNA and one RNA strand.

Methods for conducting polynucleotide hybridization assays have been well developed in the art. Hybridization assay procedures and conditions will vary depending on the application and are selected in accordance with the general binding methods known including those referred to in: Molecular Cloning, A Laboratory Manual, Second Ed., J. Sambrook et al., Eds., Cold Spring Harbor Laboratory Press, 1989 ("Sambrook et al."); Berger and Kimmel, "Methods in Enzymology," Vol. 152, "Guide to Molecular Cloning Techniques", Academic Press, Inc., San Diego, CA., 1987; Young and Davis, *Proc. Natl. Acad. Sci., U.S.A.*, 80:1194 (1983), each of which are incorporated herein by reference.

It is appreciated that the ability of two single stranded polynucleotides to hybridize will depend upon factors such as their degree of complementarity as well as the stringency of the hybridization reaction conditions.

As used herein, "stringency" refers to the conditions of a hybridization reaction that influence the degree to which polynucleotides hybridize. Stringent conditions can be selected that allow polynucleotide duplexes to be distinguished based on their degree of mismatch. High stringency is correlated with a lower probability for the formation of a duplex containing mismatched bases. Thus, the higher the stringency, the greater the probability that two single-stranded polynucleotides, capable of forming a mismatched duplex, will remain single-stranded. Conversely, at lower stringency, the probability of formation of a mismatched duplex is increased.

A nucleic acid "tag" is a selected nucleic acid with a specified nucleic acid sequence. A nucleic acid "probe" hybridizes to a nucleic acid "tag."

A nucleic acid "tag-probe" is a specific sequence capable of hybridizing to a specific "tag." Typically, the "tag-probe" is the complement or a partial complement of the "tag." In one typical configuration, nucleic acid tags are incorporated as labels into biological libraries, and the tag nucleic acids are detected using a microarray.

Throughout this disclosure, various aspects of this invention are presented in a range format. It should be understood that the description in range format is merely for convenience and brevity and should not be construed as an inflexible limitation on the scope of the invention.

Accordingly, the description of a range should be considered to have specifically disclosed all the possible sub-ranges as well as individual numerical values within that range. For example, the description of a range such as 4 to 50 should be considered to have specifically disclosed all integers within the sub-ranges such as 4 to 10, 4 to 20, 4 to 30, 4 to 40, 4 to 50, 5 to 10, 5 to 20 etc., as well as individual numbers within that range, for example, 6, 8, 15, 20, 32, 39, 43, 48 etc. This applies regardless of the breadth of the range. Likewise, a description of a range such as 1 or more, 10 or more, 10^3 or more, 10^6 or more, or 10^{12} or more should be considered to have specifically disclosed individual numbers within that range as well as higher numbers, for example, 20, 2×10^4 , 3×10^8 , 4×10^{15} , 5×10^{18} , etc.

Various patents, patent applications and publications are referenced throughout the specification, unless otherwise indicated, each is incorporated by reference in its entirety for all purposes.

II. General

The presently claimed invention provides 2050 unique sequences which have been specifically chosen according to strict criteria to produce sequences suitable for a wide variety of “tagging” applications. These sequences are provided as SEQ ID NOs 1-2050.

In one embodiment, some or all of SEQ ID Nos 1-2050 comprise tag sequences. In a further embodiment, some or all of SEQ ID Nos 1-2050 comprise tag-probe sequences. In a further embodiment, the tag-probe sequences are immobilized to a solid support.

An initial set of 2200 20mer sequences was selected with closely matched melting temperatures. A further filter based on rules such as those described in US Provisional Patent Application 60/176,520 was applied to optimize and standardize the hybridization characteristics of the set. Finally, sequences were removed if they were identical or nearly identical to each other or to sequences in the public databases. This reduced the pool of candidate sequences to 2200. The hybridization performance of the entire set of 2200 candidate sequences was evaluated. Labeled oligonucleotides complementary to the candidate sequences were synthesized and hybridized to an array containing probes designed to analyze the performance of all 2200 candidate sequences. The array contained four different sequences to

interrogate each candidate sequence. A probe designed to be the perfect match complement to the candidate sequence (PM), a probe designed to have a central mismatch at position 10 (MM), and probes designed to be the complements to the PM and MM probes (cPM and cMM respectively).

FIG. 1 shows a plot of the discrimination score and the signal intensity for all 2200 sequences. A line was fitted to select the 2050 sequences with the highest discrimination and signal intensity. These 2050 sequences are SEQ ID Nos. 1-2050.

In one embodiment of the invention, the sequences of the presently claimed invention are tag-probes attached to a solid support. Methods of immobilizing presynthesized sequences and synthesizing sequences de novo on solid supports are known. See for example, US Patent Numbers: 5,143,854, 5,242,979, 5,252,743, 5,324,663, 5,384,261, 5,405,783, 5,412,087, 5,424,186, 5,445,934, 5,451,683, 5,482,867, 5,489,678, 5,491,074, 5,510,270, 5,527,681, 5,550,215, 5,571,639, 5,593,839, 5,599,695, 5,624,711, 5,631,734, 5,677,195, 5,744,101, 5,744,305, 5,753,788, 5,770,456, 5,831,070, 5,856,011, 5,744,992, 6,040,138, 6,040,193, US Serial Nos. 09/079,324, 09/122,216, and PCT Application WO US99/00730.

In this and other embodiments it is often useful to provide control probes. As one example, SEQ ID Nos. 1-2000 may comprise the tag-probes and SEQ ID Nos. 2001-2050 may comprise the control probes. In a preferred embodiment, the control probes are representative of the population with respect to observed signal intensities and discrimination. In a further preferred embodiment, tag sequences with relatively low signals may be over-represented in the control sequences so as to increase information about the sensitivity of experiments at the lower limit of detection.

METHODS OF USE

The use of short nucleic acid sequences as “tags” to identify specific biological substances in a sample is known. For example, tags may be used as a method of or as labels for a wide variety of biological and nonbiological materials, see, for example, Dollinger, The Polymerase Chain Reaction pp. 265-274 Mullis et al., editors (Birkhauser, Boston, 1994) or as a method of screening complex chemical libraries. See, for example, Brenner and Lerner, PNAS

89, 5281-5383 (1992); Alper, Science, 264: 1399-1401 (1994); and Needels et al. PNAS 90, 10700-10704 (1993). See also US Patent Nos. 4,359,353, 4,441,943, 5,451,505 5,149,625, 5,654,413 and 5,800,992.

In addition to those applications above, the presently claimed sequences are suitable to be employed for any of the methods described in US Patent Application No. 08/626,285 (filed 4/4/96), including as a method of analysis of genomic DNA. For example, as described in the '285 application, tag arrays may be used to identify the function of identified open reading frames (ORFs) by creating deletion mutants for each ORF and analyzing the resulting deletion mutants under a wide variety of selective conditions.

US Provisional Patent Application No. 60/140,359 (filed 6/23/99) described methods of using tag arrays and the single base extension reaction for genotyping and other types of biological analysis. A set of tags and a tag array derived from Seq. ID Nos. 1-2000 and their complements are suitable to be used for the methods described in this application. Briefly, the '359 application describes methods of determining the genotype of an individual at a polymorphic locus or the frequency of alleles in a population. One embodiment of the method involves three step: (1) amplification of the polymorphic locus, (2) primer extension of a sequence-tagged primer with distinct labels for different polynucleotides at the polymorphic locus, and (3) hybridization to a tag array. The amount of each distinct label can be determined at known positions of the tag array. Each tag represents a distinct polymorphic locus and each distinct label represents a distinct allelic form at the polymorphic locus. The method permits the simultaneous determination of a genotype at multiple loci, as well as the determination of allele frequencies in a population. Another embodiment employs just steps (2) and (3).

Table 1, below, lists the sequences of the presently claimed invention. Column 1 lists the sequence ID number corresponding to each sequence. Column 2 lists the sequences in the 3' to 5' direction.

TABLE I

Seq. Id	3' to 5' sequence
1	TAAACTAGCATTGAGCCCAC
2	AAATCAGCAAACGGGCTCCG
3	GAATTGATAATCGCAGCCAC
4	GATATAGGAATGGCGCATAC

Attorney Docket No. 3108.1

Seq. Id	3' to 5' sequence
53	CATTGCGAACTGCATCTAAC
54	GATAGTCCAATGCTACTGAC
55	GATTCGGTAATGCGCTGTAA
56	GACGTTTCAATGCAGCGTAA
57	GAGAGTGCAATGCCGACTAA
58	GAGATCCGAATGCGCGTACT
59	CGAGATCCAAGGCCCATGAT
60	AGCTTGACAGTAACCATGA
61	AGAGTTGAACAGCATACCCT
62	TATCTGATCGGACGGCCAGT
63	TATTGACTACTGCGCCTCAG
64	TTGGACTATTGGGTATCGCC
65	TTGTCAGATTGGATGCGCTC
66	TATGCAGAATGGCGTGTATC
67	CATTGGATAAGCACTGATCG
68	CCCGGAATAAGGCCACGATA
69	CTCATAGAATGGACCAGATC
70	CATAGATTAAGCACTCAGCC
71	CATGATGTAAGCACGCTACC
72	CAGGAGCGAAGCAGATACTC
73	CAGAGCAGAAGCACTCACGT
74	TACATAGGCTTCAGCATCAC
75	TATTATACCTTGATCCGCGC
76	TAAACTGCTTGCATACGGCG
77	TATAAGCCTTGCAGCGGACC
78	TTTAAGCGGTGGATCTAGCT
79	TTAATAGCCTTGAGCAGCGA
80	ATAAATGCTTGAACCCCTCG
81	GAAAGTTCATGGAATCGAGC
82	GCAAGGATTTGACTCAGAC
83	CAAAGAATAATCGCTCCTCG
84	TAAAGCACTTATGACTCGGC
85	TTATAGCATTCTGTAGGCGC
86	TCGCTGACATTTGATTAGCC
87	CCTTGAATAATATCTCGGCC
88	AGGTCCAGAAATTGCTGCAC
89	AGCTCAGGAAATTCTAGCGA
90	AGCTATGCAAATTAGAGGCC
91	GGTAGGCTAATTTATGGCAC
92	CTAATGCAATTCAATGCCGC
93	CAACTGGCAATCAATACGCT
94	CCAAGCGAATGCAACGTATC
95	GCATAGCGAATTGGAGATAC
96	GCATGTCGAATGGATGATAC
97	GCACGTTCAATGGCTCGACT
98	GCAGCGCAATCTGTGAGTA
99	AGCAGTGCAAATCCTGATAC
100	AGCTTCGCAAATCTGGTACA

101 AGCCTGCGAAATCTACTGAA
 102 GCAGATCGAATTATGGAGAC
 103 GCAGAGTCAATTATCATGCC
 104 CGTTAGGCAATACATTTCCC
 105 ACTGGTGCAAAGTCTTCGAC
 106 GGTATATGAATGTGTCGTCC
 107 GATAGTGCAATCTAGGTGAC
 108 GCAGTGCAATGGATGTACTA
 109 GCTAGGCTAATGTCCGGCTA
 110 GGTAGCCTAATGTGTGCTCA
 111 GGACGTGCAATCTTGTGACC
 112 GAGCGCCGAATCTAGTCGAA
 113 GGGAGCGACCTCTAGCTTAT
 114 GCGGGTCGAATCTCGCTTAA
 115 CGCCGCGCAAGCTGTATTAA
 116 CGGCTGCGAAGCTGTCTTAA
 117 CATCCGCTAAGATCGGTAA
 118 CGTGCGAGCATAATCCATCAG
 119 TGAGAGCTGGATCGCATTCC
 120 TAGGTGCTAGGATCTCAGCC
 121 TAGGTATCAGGATTCAGGCC
 122 TGCGCCAGTGAGTCGTATAT
 123 CAGCAACGTGGATCAACTAT
 124 CAGCGGCTAAGATCAATACC
 125 GCAGCCTAATCTGGCCTAGT
 126 GGGCCTGTACCTGCAATTCA
 127 TAGGCCGGACCTGCTGTTAT
 128 TAAGCCGCCACGGAGTGTTA
 129 TAAGGCTCTTGAGACGTAGT
 130 TAAGCCCGATCAGCATGGAC
 131 TTGCCCGTAGTCAGCTTAGA
 132 GAAGCACCGATCAGACACTG
 133 CAGGCACCAAGTAGCACAGT
 134 GGTGCGCCATGTACTCAGTT
 135 TCAGGCTTATCGAGCGCGTT
 136 GCAGGCAGATCGACCTAGTT
 137 GGATAGGGACTCAGATATAC
 138 GCATGGTTACCTACGCCAGA
 139 GGAGGCTGACTCATACGCAA
 140 GGAGCCTGACCTAGTCGATA
 141 GCGGCCAATTCGGCGATAAT
 142 GGTGCTCGACATTAGGCCAT
 143 GATCCACATAGCGGACAAT
 144 GATCCAATCTGTCAGCACAT
 145 GAGCCAATCTGACTACCAGT
 146 TGCTGGATATGACTGTCGTA
 147 TGCTCTGCACTGCTGACGTA
 148 TCACCAGCCAGACTGTGTAG

Seq. Id	3' to 5' sequence
101	AGCCTGCGAAATCTACTGAA
102	GCAGATCGAATTATGGAGAC
103	GCAGAGTCAATTATCATGCC
104	CGTTAGGCAATACATTTCCC
105	ACTGGTGCAAAGTCTTCGAC
106	GGTATATGAATGTGTCGTCC
107	GATAGTGCAATCTAGGTGAC
108	GCAGTGCAATGGATGTACTA
109	GCTAGGCTAATGTCCGGCTA
110	GGTAGCCTAATGTGTGCTCA
111	GGACGTGCAATCTTGTGACC
112	GAGCGCCGAATCTAGTCGAA
113	GGGAGCGACCTCTAGCTTAT
114	GCGGGTCGAATCTCGCTTAA
115	CGCCGCGCAAGCTGTATTAA
116	CGGCTGCGAAGCTGTCTTAA
117	CATCCGCTAAGATCGGTAA
118	CGTGCGAGCATAATCCATCAG
119	TGAGAGCTGGATCGCATTCC
120	TAGGTGCTAGGATCTCAGCC
121	TAGGTATCAGGATTCAGGCC
122	TGCGCCAGTGAGTCGTATAT
123	CAGCAACGTGGATCAACTAT
124	CAGCGGCTAAGATCAATACC
125	GCAGCCTAATCTGGCCTAGT
126	GGGCCTGTACCTGCAATTCA
127	TAGGCCGGACCTGCTGTTAT
128	TAAGCCGCCACGGAGTGTTA
129	TAAGGCTCTTGAGACGTAGT
130	TAAGCCCGATCAGCATGGAC
131	TTGCCCGTAGTCAGCTTAGA
132	GAAGCACCGATCAGACACTG
133	CAGGCACCAAGTAGCACAGT
134	GGTGCGCCATGTACTCAGTT
135	TCAGGCTTATCGAGCGCGTT
136	GCAGGCAGATCGACCTAGTT
137	GGATAGGGACTCAGATATAC
138	GCATGGTTACCTACGCCAGA
139	GGAGGCTGACTCATACGCAA
140	GGAGCCTGACCTAGTCGATA
141	GCGGCCAATTCGGCGATAAT
142	GGTGCTCGACATTAGGCCAT
143	GATCCACATAGCGGACAAT
144	GATCCAATCTGTCAGCACAT
145	GAGCCAATCTGACTACCAGT
146	TGCTGGATATGACTGTCGTA
147	TGCTCTGCACTGCTGACGTA
148	TCACCAGCCAGACTGTGTAG

Attorney Docket No. 3108.1

Seq. Id	3' to 5' sequence
149	AGGAGCAACCATCATGCACG
150	GGGCATACCTATCCCGAGAT
151	CGGGCGATACCACTCAGATT
152	AGCGGCAACCAGACATACGT
153	CACGCCATACCAAGGAGAGT
154	CAGTGCATACCAAGCGACGA
155	CAGGCAGTACACAATCTACG
156	TACGTCGCATCCATAGCTGA
157	GAGTGACACCTCAGCAGATA
158	CTACAGCACCTCAGGAGAGT
159	CTCACGACATCCAGGAGTAT
160	CCAGCACGACAGAGAGATGT
161	CGCACACACCTGAGAGAGAT
162	GCGCACGCACTCAGATGTAA
163	AGACGCTCAACCACGAGAGT
164	GACGCCACAGTCACTAGAGA
165	GGCGCACACTGTACTCAGAT
166	CGAAGCGCCAGTACCAGATA
167	GGGTCGCTACCTACTCTGAT
168	GAGACATGATCTACCAGTAC
169	GGACGCTTACTCAGCAGTCA
170	CGGGTGTTACAGAGCTATCA
171	CGCGGCTTACACAGACATTA
172	CGGAGCTTACACATTAGCAG
173	CTGAGCATACACTTCACGAT
174	CCGATCATAACTGTAGATGC
175	CCGCCGATAACTGCTTGAGA
176	GGCCATATACGAGATGTAGA
177	CGTCCCTTAACGGCTGGTAT
178	ATACCCAGAACGACTATGCG
179	ATCCCACGAACGATGAATCT
180	ATCCGCAGAACCGGCGATAA
181	CCTCGCCGAAGCGTGTTTAA
182	GCGCCGCACAGAGTCTTATA
183	CGCGCTGCACAGAGCATATA
184	CCGCTGACACAGGCAGATAT
185	GCGTATGACCAGGTGTATAT
186	CTGTATGAAGGTGCTGTACT
187	GTTTCGCACGAGGATGTATC
188	GTGCTCGCAGAGGATTTATC
189	TAGGCCAGAGTAGCGACTTA
190	CAGATCCTAAGAGCAGTTAC
191	TAGATGCTAGGAGCGATTCA
192	TAAGTCGGTGGAGCATATCA
193	TAAGCGCGTGGACTCCTAAA
194	TAAGTGGACTGAGCGCATAT
195	TATACGGCAGTGGATCAGAT
196	CTATACGCAATGCACTCAGA

אנו מודים לך על שיתוף הפעולה שלך. אנחנו מודים לך על שיתוף הפעולה שלך. אנחנו מודים לך על שיתוף הפעולה שלך.

Seq. Id	3' to 5' sequence
197	CTATCGTCAAGTGATGGACC
198	TATAGACTAGGTGATCGAGC
199	TAGTACGAGTGGGCATCAAA
200	TAGACGTAGTGAGCATGACT
201	TGACGAGTTAGGATCTATGC
202	TTACGAGTGTAGCGTCCATG
203	TCGTCGTAGCATCTCGCAGT
204	TCGACGTAGGATCGCAGTAC
205	TCAGTATCATGGAGTACGAG
206	TGCACTAGATGGGATCGACT
207	TGCGATTACTGCCGTCACGT
208	TGGA CTCTATGGCAGCCGTA
209	TGACAGCAGTTGCAGTCCGT
210	TACACAGGCTTGCAGCTCGA
211	TGCAGCGGAGTGCCTCATT
212	GCGCAGGGAGATCCATATCA
213	CGGCAGCCAAGTCCAGTATA
214	CAGCGCCCAAGACGTGTATA
215	GTGCCTGCATAGCGATAGTC
216	TGCCTGCGAGAGCCTGTATT
217	TGGCATCGAGAGCCGTTCTA
218	GCAGGAGCAGAGCTTATATC
219	GCGGGATCACGACGTTTACA
220	GTGGCGATAGAGCATTCTCC
221	AACGCGAGAAACCATTGCG
222	AGGCAGACAACCTCAATCCGG
223	AGGAGAGCAACCTACACTCG
224	AGCCAACGAACCTACATGGG
225	CCGCAAGCACGTCGAATGAA
226	GCGCATGGACGACAAACGTA
227	GCCAGGAGACGTAGATATTA
228	GCGCATAGAGAGAGATCATC
229	TGGTATATCGGTAGATTCGC
230	GAGCTATAAGGTGGATTCAC
231	CGCGGATAACTTGATTCACC
232	GTCGGCTTACCTGATAGCGA
233	GGAGCTATACATGCCTATCC
234	GGTGCCGTACATGCTCGTAT
235	TCGGCTTGACGTGCTCGTAT
236	GGGCTGTGACTAGACTCTCA
237	GCGAATTTAGTAGACGCACA
238	GAATCTCGAATAGCGGTACA
239	GACAGTTGACATGACAGTAG
240	GACATTGACATCGCATACAC
241	GAGTTTAGAATCGTGAGCAC
242	CTATTCGCAAGTGTCGAGCC
243	GTTATGGACACTGCTCGACG
244	AGCGTTCTAAATGCGTCACA

Seq. Id	3' to 5' sequence
293	GTTATCTACGGATCATGCGA
294	CTGCCGTAAGTCTCATGCGA
295	CTAGCCGAATACTGCATACA
296	CTGCGTCGAGAATCGCGTTA
297	CATACACGACAATAGCTTCG
298	GATACCGACTCATACATTGC
299	GATACCGCACGATCAGCAGA
300	GTATATGCAGACTACTGGAG
301	TATAGTCGATTATCCCAGCC
302	CATAGTACAATATCCCGACG
303	CTTGACAGCTACTACCA GTG
304	CTGAGACAGCTATCGACACA
305	CTGAGTAAGTCTTCCACACG
306	TCGGATATACTATGCGTCAG
307	CGTAGGATAGAATGCACAGT
308	CATGATACACACTCACGAGG
309	CGGAATCACGACTACATACG
310	GGGTATCACGAGTCACCTCA
311	GAGAGAATCGTATCACAGCC
312	GAGTATGTAATCTACCTGCC
313	GAGTAATCATAGTAGCAGCC
314	GACTATATCCAGCACCGAGG
315	GACATATAGCTCCACTCAGA
316	TAGACCTAGTTGCAGCGCGA
317	TACTACACGTTTCACGGCAG
318	GTACATATCTGTCACGCGCA
319	TAGTATATCCTACGCCGCTA
320	GAGTATATCGCAATGCCAGC
321	GAGTTGTACATAGGCCACC
322	GACGCATGACATATTCCTAC
323	GAGACACTTGACAGTAGCCA
324	GGCTAGTTACTCAGATCACA
325	CGCAATAAGTCTAGCTCACT
326	CATGTACTAAGCAGTCACAC
327	CTAGTTAATGTCAATCCGGC
328	GACTGTGTAATCATTGCAGC
329	CGTTCGTGAATCAGCACAGC
330	ATTCGGTCACACAGCACAGA
331	ATCTGCTGACACACACTAAG
332	AGCTCGCTAAATATGTAGGC
333	ACTGTCGCAAATATCACACG
334	ACTGTCTGACCAACCAATAG
335	GTTACTAGCTGGACCTCAGA
336	TTATAGACTGGTGCGGAACA
337	TTAGCATACTGTGCGCGAAC
338	TGTGCTGACTTAGGTCGAAT
339	TCTCGGGACGTTGCGCTATA
340	TGTCCGCGACGTTGGCTATA

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Seq. Id	3' to 5' sequence
341	TGTTCTGACTGTGCGCTAC
342	TGTCAGGTACTGGTCGCTAC
343	TTTACTAGAGTGGCGCATGA
344	TTTACTAGAGTGGCGCATGA
345	TTAGATAGATGTTTCGGCCAG
346	CTCAATAGATTATAGGCGCG
347	TCGAATCGCTGTTACGGAAA
348	TCAGACTAGGGTAGCGCATA
349	TCAGCAGTATGTAGGCAGTA
350	TAAGCCGGGTACGCTATTT
351	TATGACCGATGTGCAGGTAT
352	TTAGCACGCTCGGCGATGTT
353	TTACACGGTCTGCGAGCTT
354	CTTCAGACAGGAGGAGATAT
355	TCCAGCCGACGTGCGATTTA
356	TCCAGCGTACCTGCTTGTAG
357	CTCCAGTCAAGTGCTTCGAG
358	CTCCAGCGAAGTGATGAGAA
359	TGTCAGCGGATCGCCATATA
360	TCCATGCGAGGATCAGGTAT
361	TGCAAGCAGTTCTCAGCGTA
362	TGTAGGACCTGTGCTCACTG
363	TTTATCGCAGTGCTCAGGCT
364	TATGTCAGCAGGCCAGCTT
365	TTCTCGTAGCTGCGCCTAGT
366	TATTCGAGCTAGGGACGCAT
367	TATTTATACTGCGAGCGAGG
368	GACCTTACACTGGCACGAGA
369	TACTGATAGCATGGGACGTT
370	TCGGATAGCAGTGCGCTCTA
371	GCTGATGCACGAGGCCATTA
372	GCTGGATCACGAGGCTCATA
373	CGCTTTGTACCAGGCCATAG
374	CGTGATTGACCAGACCCAGT
375	TACGCTGGATCAGACGGTCA
376	ATCCTGAACGCAGAGACACG
377	ATCGTTGCACCAGAACTACA
378	CTCTCAGGACCAGCATGATA
379	TCTGAGCGATCTGCCAGTCA
380	GGTGAGACCTATGTATATCG
381	TTAGAGTCTTAGGCATGTCG
382	TTATAGCCGTAGGCAGGTAC
383	CTCTAAGTATTGGACACGCA
384	GCTAGGATATAGGACACTGA
385	GCTATCGAATGTGCAGTACG
386	TCTATCCACTGCGGACGAGT
387	TCATACTCATGTGCAGCTCT
388	TCATCGAGATCGGCCACTGT

Attorney Work Product
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Seq. Id	3' to 5' sequence
485	TGAGTAGGCAGTCCGATCTA
486	TGATAGGCAGTGAGTTCATC
487	TTATGGCGAGAGTTGTCATC
488	GTTTAGGCACGATGCTGTAT
489	GCGTTAGGACCATAGTCTAC
490	CCGATGCGACAATACGTTAG
491	TCTAGCGTCCCATAGCGTAG
492	CTGTCTGGACCATAGCAGCA
493	CTGCTTGACGATGAGCGAA
494	TAGCCCGGACGATGTAGTCA
495	CCGCTACAAGCATTGGGAAT
496	CGGCTAGAAGAATGAATGCT
497	CCGATGATAAGCTAGTATGC
498	GCGGATAGACCATTATTGAC
499	GCCACTAGACCATCGGTGAT
500	GCACGCGGACCATCGTTTAT
501	GCCGCTCGACCATAGTGATA
502	GCCGAGTCACCATGCTGTAT
503	CACGGGTCACCAAGCGTATT
504	GACGGCGACCCAGGTTATAT
505	TGTGCGTCAGCAGTTAGTAT
506	GCTCGGCTACCAGTCGTTAT
507	CGCTGGACACCACTGTGATA
508	CGGTGGAGACCAGATTATAT
509	CGCGGGACACCAGCATATTA
510	GCTCGCGCATTAGCATATAA
511	GCTGACATCCACGCATTGAG
512	CGCTGATCCACCGAGATTAG
513	ACGCAACCAACAGCGAGTGT
514	CACAGACCACAAGCTATGGG
515	CCTAGCCCAAGGCATTAGAA
516	CCGTAGCTCCAAGGCATGTA
517	CAGTGCGCCAGAGCAAGTAA
518	GAGCCACCACGAGTCATGTA
519	GGTCACCACTCAGCGATGTA
520	GTGTGCCACTAGGCCGATTT
521	GGAGACCCGTAGGCATAATT
522	CGCTGTAAGGATGCTGAATA
523	GTCGTGCAGGATGCCATATT
524	GTTCCGCACGATGCCAGATT
525	GCTGCGACCATCGTCAGATA
526	GTCTAGCGATCATGCTCAAT
527	CTCTACGAATCATGCGGAAG
528	CTTAGATACTACGAGCACGA
529	GTGACGCTACGTGAGCCTAA
530	TACCGTGTACGTGAGCGCAT
531	TACTGCGACGTAGCGAGTCA
532	TACTAGGTACTCGCGGCACT

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Seq. Id	3' to 5' sequence
581	GTATATGACCTAGTGCCACG
582	GTGTTGTACGATGTGCTCCA
583	GAGTCTGACATAGGGCACCT
584	GAGTTGCACGTAGACGATAC
585	GA CTGCGCATAGACACATG
586	GACAGGCTACGAGACTAGAT
587	GTGACGGCACTAGCAATATA
588	CTGCTCTGACACGCGAGTAT
589	CGGCTGTGACACGAGCTATT
590	CTGGTGCGACACGCCTATAT
591	GTCAGTGGACTAGCCCTACA
592	ATCGAGTCAACCGGCCTAGA
593	TCGATAGCCTACGTGCCGTT
594	GGAGACCTCTACGCACTGTT
595	GCGTGACAGCTCGCACTATA
596	GCGTAGCTCAGCGACATTAA
597	GCTATACGCACCGTCATGTA
598	CGCATACACTCAGCAGAGAT
599	CTACTTACAGCAGCGACGAG
600	ATCTCGACACAAGCTAATCG
601	CATCGGATACACGCATACAG
602	ACATACAACACCGCTTAGGG
603	TACTGAGTCCACGCTCGGTA
604	GATACAGCCTACGACCGGAT
605	GATACATTACTCGACACGCG
606	CGCTACAGAGATGCACAGAG
607	CCGACTGTA ACTGCGATGAA
608	GGTGT TATACGTGCATAGCC
609	CTCGTATTAAGTGCGCTACC
610	TATAGTATCGAGGAGCGACC
611	GTATAGTACGTGATAGGCTC
612	GTACGATACGTGACTAGAGC
613	GTAGGTCGAGCTGCATACTC
614	TTACAGTAGTCTGCATCCCT
615	CTAGTCAAGTCTGCATACAG
616	CTGTCTAATACGGCCACATA
617	CTCGCAATACGTGTACCGTG
618	TCCGATCTACGTGACGGTGA
619	TCTCGCCGACGTGGTCTTAA
620	TCTGTCCACGTGCGGTTAT
621	TCGTCCTGACTCGCTGGTAA
622	GTCCCTAGACTCGCAGTGAT
623	GCGACAGTAGCTGCAATGAT
624	GACGTAATATCGCCACATCA
625	GACGAGGTACAGCGCATACA
626	GCAGGTCTACGACGCATGAT
627	GCAGAGTACGGACGCATATC
628	GAGTAGATACAGGTCACGAT

Attorney Docket No. 3108.1

Seq. Id	3' to 5' sequence
629	GAGCGATCACACGTCCGATT
630	GGTCGCATAGACGTATCAGT
631	GGTGTCTCACGAGTATCGAC
632	GTAGGCTAGACGGTCCACTA
633	GACGGACACTGAGCACATAG
634	GACACCTATGTAGCAATGAC
635	CACAGTACAATAGCACCTGG
636	CACCAGAACGTAGGCACAGT
637	CACTACTCAAGAGCCAGTTA
638	CGCCGACGAATAGCCAGATA
639	GCCGCACTACTAGCGATGAA
640	GACCAGTTACGAGCAGCGAA
641	GATCACGTAGGAGCACCGTA
642	GTACGCAGAGGAGTCATCCA
643	GTCGCTGACTAGGATCACGT
644	TACGCAGACTCGGACTCGAT
645	GTCGCTATATCGGACCTAAC
646	ACTCGCATAAACGACAGTCT
647	TGGAGTCGAGTAGTACATAC
648	TACGACATGGTAGGACGCTA
649	TGACTTCTACGTGGCGATAT
650	TACGCTCCGAGAGGCGATTT
651	CACCTTCGACGAGCAAGAGT
652	TACGCTCGCTCAGCTTAGGT
653	TACGGCATCGACGCTATTGC
654	TACGGCGACTGAGATGCCAT
655	TACGTGCTAGGAGATGTAAC
656	TATCGTCTATCAGATTGCCC
657	TATCGTATCCACGTTCCGAG
658	GATCGTACATCAGTGTCCAC
659	GAGTCTATATCAGTAGCGAC
660	GTTAGTCGATCAGTAGAGCA
661	GTCCTACGATGAGTGACGCA
662	CGTCTTCTAAGCGTGCTGAA
663	GTCTCCTACCGTGAGCAGTA
664	ATCTCACTACAAGAGCCTAG
665	CTGTGACGACCAGACGCTTA
666	CTGAGCGTAAGTGATTGTAC
667	CTCGTAGCAATAGATTTCCC
668	CTACGTGCAATAGCAGCTCA
669	CCGGCAGTACAGATAAGTCA
670	CGCCGGATACAGAGTAATCG
671	CTCAGCATACATAGTACAGC
672	CCGAGCTTACAACGTGTGCA
673	GACGCATTACCACTGGCGAT
674	CAGGGTGTACCACGAAGCAT
675	CGGTGTTTACAGCAATCCAT
676	CTGGCTGCAATAGCGCGATA

Seq. Id	3' to 5' sequence
773	GTTGCGCCATTGAGCCAGAT
774	GTTGCCACCTGAGACGTTA
775	AATGCGCCACAAAGCGAGTG
776	CACCGGCCAAGAAGTACAGT
777	CATCCGCCAAGCAGAGTGAA
778	CGTTGCCAATGCACGAGCTA
779	GATGGCTGAATGACGTTTAC
780	GATTGCCTAATGAGTCTGAC
781	AATCAGCCAAAGATGTGGGC
782	AATCATGCACAAAGTTCGCC
783	ATTTAGGCAAGAAGCGCACC
784	AATTGGCTAAAGAGCGCACC
785	ACATTGGCAAAGCGAACTCC
786	AATGGGAGAAAGCCGACTCT
787	TGTGCTGGAGCTTCAGTCAC
788	GTTGTGCAGGATTATCGACA
789	GCTTGCAGACGAGTCATCAC
790	GGATGGATACTAGCGACTCC
791	GCTATGGCACAGGCATCTAC
792	GGACTGGCACATCCCGTATA
793	GGATCGGACCATTCTCACTA
794	GGATGGCGACATGCTCACTA
795	GAGCTGGCAATCGTCGTACT
796	GGATGGCTACATGATCTGAT
797	GGCAGCAATTCGGGCTAATA
798	GCCTAGCAATGTTCCCAGAG
799	GAGCGGCAATGATGATCCAT
800	TGGTGCATAGCTGCGATCCA
801	GGCTGCACAGGTGTATCCAA
802	GAGATGCCAATCGGCCATAA
803	TATATGGCACATCGTTGCGA
804	TGATGCCACGTCGTCTGAT
805	ATTGATCCACACACAGTACG
806	AGCTGATCCAAGCAACGTAC
807	GTTGATGCAGATCGCGTATC
808	TCGTGGGCAGATCGCTTCAT
809	TGTGGCCGAGATGCCTTCTA
810	TTTGCGGACTTCGCTATCAA
811	TCCCATGCACCTGAGTGGAT
812	TTTCATGGAGCTGTCGCGTA
813	TTTACCTGTGGTGATAGCGA
814	TTGTCATGCTGCCAGTCGA
815	CTTTCATGCAGGCAGAGCCA
816	CCTTTAAGCTGGCACACGAT
817	CCTATCAAGGATGCACACGA
818	CCGTCAGAATATGACACAC
819	TAGGTCAGATCATGCGCGAC
820	ATGTGCATACAAGCTACGAC

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Seq. Id	3' to 5' sequence
821	CTGAGAATATGAGAGACGCC
822	ACTCACGCAAATGAACGGCG
823	CTTAGCGAATATGCGATACG
824	ACTCTGATAAATCCGACACG
825	ACTGTGCGAAATCCCAGACA
826	ACTGATGTAAATCCACACCG
827	ACGTGAACAATTCCACACTG
828	ACTGCACGAAATCGACATCG
829	ACTTCTGTAAATCGCAGCAC
830	CTGTCTTGAATAGCGATCAC
831	ATGCGGTTAAGCGGTAATAC
832	TACGCTGAGTCATCCGAATA
833	CTTGTGAGACACTCCGACAT
834	CTGGTGACATACTATCAGAC
835	CGTGCGTTAAGCTGTCGATA
836	CGGTATCGAAGCTGTGCTAA
837	CGCGTGTGAAGCTGCCTATA
838	CCTAGTAGAAGCTCCACAGA
839	TGTGTGCGGAGTCGCCCATAT
840	TCTGTGCGAGGTAGGCCATAT
841	GCTGTGCGAGAGCGATCATCA
842	GCAGTCGGACGAGATTCTAC
843	GCGATGGTACTAGATCAGCA
844	GTGTAGGGACTCGTATCACT
845	GTACGAGCAGTTGAGCATAA
846	GTCAGTCGAGATTCAGCAGT
847	GTCGAGTCAGATGCACGTCA
848	GTGTATCTAGCTGCACGCAC
849	GTTGTCTTACGTGCAGTCAG
850	TATGTACTCGTATCGACGCA
851	TCGTGTGCGAGTATCCGCAA
852	GTACGTTGACAGTCTGCACA
853	TTCGTAGAGGTCTGCCAATT
854	ATTCTGAGAGACAAGCCTCC
855	ATTCTGACACAATCATCGCG
856	ATTCAGAACTAATGCACCGC
857	AGGTATGAACCATCGCACAC
858	ATTTGATGAACTCCGCAGAC
859	GTTTGCTGACCTCGCAGTCT
860	ATTGCCGGAACGCATTATAC
861	TGTGTGGGATCGCCCTATCT
862	TTGAGTGAGCTGCGCTTATA
863	TGCGTGCAGGTGCCACTAAA
864	GTGCTGCATGAGCCAGTTCA
865	GGCTCTACATGGCGATAGCA
866	GCTCTCTAATTGCGGACACA
867	GGATATAAGTTGCGGCACTA
868	GGATGTAATGGTAGCTCCTA

Seq. Id	3' to 5' sequence
869	GGATGACGAGGTCTCACCAT
870	GGATGCGACGATCTCGACAT
871	CGTGATCGAAGGCTGCACAA
872	CTAGATGTAAGTAGCTGGAC
873	CGAATGAAGGATCGAGACCT
874	CGGCCTGGAAGTCACTCATA
875	GGCCTTGGACTACCGCTTAA
876	TGCTTCGAGGGTCCCACTTA
877	TGCCTGGTACTGTCCGACTA
878	TGCTTGTGAGAGTCGCTACT
879	ATGCTTGCAGAACCCTCAGC
880	TGACTGTAGGGAGCCTCAAC
881	TGCTTGGCAGGATGTCTTAA
882	GGCTCCGGCATGAGTATATC
883	TGCTTTGCAGTGAGGCTCTC
884	CAATTTGGAAGTAGCCTTCG
885	TTTGCTGCATCCGGCCTGTA
886	TTGGGGCCACTGCGCTCTTTA
887	TGTGAGCCCTTGGCACGTTA
888	GGTGGCCCGATCACATTCAA
889	GGCAGGGCACCTCAGTTTAT
890	GGGTGGCCCATGCTATCTAA
891	GTCTGGCCCTACCTATGGTT
892	GCGGGCACACCTCTGATTTA
893	GCGGGCGCACCATTCATTAT
894	GGAGCCCACCATGAGCTATA
895	GAATCTCCACCAGGCGGATA
896	GGATACGTGCTACAGTGAT
897	TCGTATAGCTGTATCGACGG
898	CTAACTAGCTGTAAGCGACC
899	ACTAGATAACAGATGCGCCG
900	CAACTATCATCAAGACGGCG
901	CAACAGAGATGAAGCGCGTC
902	CAACATATCATAAGCGCGTC
903	GCAGATAGCATCATATACGC
904	GCAGACTGAATTAGCTCTAC
905	GTTAATTCATCTAGCGCGAC
906	AGGAATCTAACCACGCGCAG
907	AGACCAATAAGCACCCCTGGG
908	AGACAAACATTACGCGCGG
909	AGAATAAATTACTGCCCGGC
910	GAGCACATATTATTACGCC
911	CAGAAGATAATATGCTCGCC
912	GAATAGCCGATAATCTCAGC
913	GAATAGCTTTACACTGCCCT
914	GAATCACTCTGAATGAGCAC
915	GGATCACACTGCCGGAATAT
916	GGACCCATAGCACTCTGATT

Case 1:18-cv-01000-UNA Document 1-1 Filed 08/01/18 Page 1 of 1

Seq. Id	3' to 5' sequence
1013	CGATGCGCCACTCAAGGTAT
1014	TATGCCGACGGTCAGGCTAA
1015	TATCGCCACGTCCGGTGATT
1016	TCTCGCTCACTGCGTATGAT
1017	TATCCGTCACTCCGTAGAGG
1018	TATCGACTATCCCTGAGACG
1019	GTATAGACCTCTCAGACGCG
1020	CTATCGTAATATCAGTCCGC
1021	CGATGACAATTAGGTACACG
1022	GAGCATAATGACGTAGACCG
1023	CGACAATACTTGACAGCACG
1024	CGATGATAATAGAGTAGCCG
1025	CTATGATTAAGTCGTAGCCC
1026	AGGTGAATAACGCATACGCC
1027	GAGTGAGTAATGCTACGTCA
1028	GATCGACGAATGTTAGAGAC
1029	GACTCACGAATGCGGAGACT
1030	GACCGTCAATCGCGTCAGAT
1031	TACCCGCATCGACGGAGTTT
1032	GTCAGCGCACTCCTGGTTTA
1033	TCAGGCCACGTAGCGTTAT
1034	TTGCGGCTATCCATGCGTGA
1035	TGCTGATACTCGGCTGCATC
1036	TGAGTAGCATCGGTGACTTC
1037	TTGTATCACTGTGCTGCCCA
1038	TTTAGTCAGTATGCTCGCGG
1039	TTACGTTTATATGGCCGAGG
1040	TGAGATCACGTTGCGCGAGT
1041	GTATCATTAGCTCCGCAGAG
1042	TATCATGTAGACTCGGAGGC
1043	GTATGCTTAGATATGCAGCG
1044	TTGTAGTTAGCTCTGCACGG
1045	ATATCGTTAAGCCATACGCC
1046	ATTCTGATAACGCTCTCGAC
1047	ATTCGTCCAACGCGGTCGAT
1048	ATATGCACAACGCGCAATCG
1049	TTAGCTCTATCGCAGTCCGA
1050	ATTAGCTGAACGCCTCGCAA
1051	ATTATCTCAACGGAGGAGCA
1052	ATGTTGCTAACGGACGGACA
1053	ATGTGTTCAACGGAGACAGA
1054	CTCTTTCTAAGTGAGTCGAG
1055	CTGCTTGAAGTCGTCTCACG
1056	CTGCGTTGAAGTGGCTTACT
1057	GTGCGTTCACATGGCCGTAT
1058	GTAGCCGCACCTGACTGTAT
1059	GTAGCGCCACCTGACGTTAT
1060	GGCGCGTCACATGATACATT

Seq. Id	3' to 5' sequence
1061	GGTTGCTACGATGACTCAGT
1062	GAAGGCCCGTACACTCTATA
1063	GACAGGGCACACGACTCTAT
1064	TGCGCGGCACTCGTTCTATA
1065	GCGGTTGCACTCGTAGCATA
1066	GAGGCGTGACCAGTCCATAT
1067	GGACGCTCACCAGTGCTTAT
1068	AGTGTCCAACCAGACCAGAG
1069	AGTGCCATACAAGCGCATAG
1070	GTAGCCTTACATTGGCAGAG
1071	GTCGCCGCACATTCGGTTAT
1072	GTTGAGTCAGATTAGCAGTC
1073	TCGTAGGGACTGCGCTCATA
1074	CTCAGATGACAGCGACGCAT
1075	CTCTGAGGACAGCCGAATCT
1076	CTAGGATGACAGCCAGACAC
1077	CGTGAATTACATCAGACAGC
1078	CTGATTATAGCTCATACGCC
1079	CTAATATGATGACAGTCCGC
1080	TACTTATGATGACTGCGGAC
1081	GAACTATGCTGACAGTACCG
1082	CGATTCTGACCACATACGAG
1083	CTAATCTGACCACGAGACGA
1084	CTGTATTGACATCAGACGAG
1085	CTTCTCAGACATCGGACGAG
1086	GCACTGTGAATTAGCGAGCA
1087	GCCTACGGAATTGGCAGACT
1088	GACCTGGAATTAGCACACGC
1089	GCCTGCGAATTAGCGGACAT
1090	GCGATGCTAATGATGTGTAC
1091	GCCCGTCTAATGAGTGGACA
1092	GCCTAGCTCATCAGACGGAA
1093	GCATGGACATCCTACGAGAA
1094	CGCCTGCCAAGCTGTGATAT
1095	GCCTGCGCCATCAGTAGATA
1096	GCACGGCCAATTACTCGATA
1097	GCAGCGAGACCATGTGATAC
1098	GCAGCAGCACACTGATCGTT
1099	GACCCAGCACATTAGCGAGA
1100	GCTCCTGCAATGTGCGGATA
1101	GCGCCTGAATTGTAGCACGT
1102	GCCACAGCATTGGAGAGAAT
1103	GCCAGGCTAATGGATAGTAA
1104	GCCCTGCGAATGAAAGACAT
1105	GCAGCGGGAATTAGATATAC
1106	GCAGGTGCAATGATTCTACC
1107	GACCGGGCAATCACTTCAGA
1108	GCCGGGCAATGCGTTCATAT

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Seq. Id	3' to 5' sequence
1109	CCCAGGGCAAGCGATCATAA
1110	GCCACAGGCAGGGCATATTA
1111	GCCTAATCCTGGGACACTGA
1112	TCGTCTCGATCTAGGCCATG
1113	GTGTCTCGACTCAGCCTATA
1114	GACGTAGTAATCATGTCTCC
1115	GACTIONACGTCATGCGACC
1116	ACGATGTAACACAGCGACCG
1117	AGTCGTGTAACCATGTGACA
1118	GTCGTGACAGTGATGTACTC
1119	GTGGAGTGACGTATCTCTAA
1120	TAGAGGTGACGTAGTCCACT
1121	GTCGTGCGAGATAGCTCTTA
1122	GTGTAGAGATATAGCATCGC
1123	TAGTCGTGAGATAGCGATTCT
1124	CAGTGTGTACGAATACGAAG
1125	CGAGTGTCACATACCACATA
1126	CGTATAGCAGACAGCGCAAT
1127	GACATCGACGACAGGCCATA
1128	CGAAGCTCACGTAAGTCAAG
1129	TAGTGCTCACGTAGCCCAGT
1130	TGCCCCACGGTGAGCTAGTTT
1131	TAGCTGCCAGGAGCGTTCTA
1132	TCGGCCTACGCTGTGCATTA
1133	TAGGGTACTGATGAGCACTC
1134	CTACGGGAAGGTTAGCACCA
1135	TGGTGATACCTGTGCGCCTA
1136	GATTAGATACCACTGCCACA
1137	GGAGTGATACCTCGATCCAC
1138	AGCTGACGAAATCTTCACAC
1139	GAGGAGATAATGGTCACTAC
1140	CACGGAATAATACATCCTCG
1141	ACAGCAACAAGTCGAGCCGT
1142	ACGGAGAGAAATCAGCCCTC
1143	CAAGAGATAATACGGCTGCC
1144	CAAGTCCTAAGACAGCTACG
1145	ATAAGCGCAAGACAGGCGTC
1146	ATCTGAGCACAACCTAGGACG
1147	CACAGGCTAAGACAGGAGCT
1148	CATAGCGTAAGCCAAGCAGC
1149	CATAGTCTAAGCCACATCAG
1150	GACAGTACATGCCAATCAGC
1151	GCGGTAATCGGTGCATCAAA
1152	GGGAGTATAGCTGACCATCA
1153	GTAGGCAGACCTGATCCCTT
1154	GAGCCAGACCACGCTTGATT
1155	GGCGCATCACTAGCCAGATT
1156	GGAGCTACATCCGCCAGTTT

Seq. Id	3' to 5' sequence
1205	GACGCGAGATCAATGTAGTA
1206	CGAGAGTAATCAATCATCCG
1207	CGAGCAATACATACATCTGC
1208	CAACATAGTTACACACGCTG
1209	CAGCTTATAGAGACACACTC
1210	CCATAGAAGTAGACACCTCG
1211	CTCAGAGACATGACACTCGA
1212	ATCAGGTCAACTAATCACCG
1213	AGCGCAGTAAATAGCTTAGC
1214	ACTCCACGAAACATGATTGC
1215	CTCAATATAGACACGATGCC
1216	CGCATTAGAGACAGATCGAG
1217	CGCACATGACATAGAGCACG
1218	CGCACATTAGACAGAGAGGC
1219	CTAGACTAATGCAGAGAGCG
1220	GCGTATAGATGCAGAGATCC
1221	TCACTAGCGTGGAATAGAGC
1222	CAGACTGAACTCAATGTACC
1223	CACGATGAACTAGATGTACC
1224	CGAATGATAAGTATGACGGC
1225	CGAGATGCAAGTATAGTACC
1226	GGATAGCGAGATATAGACCC
1227	GCATAGCACGATGGACGATC
1228	CTCACAGGACATGCAATCGG
1229	TATACATGCTTCGATCACCG
1230	ATATCAATAACTGCGACGCC
1231	AATACGAAAGATGCGGCCCG
1232	ACAGATACAAATGTGCCCCG
1233	ACGAATAGAAATGTGGCCGC
1234	ACATTACTAAAGGTGCGACC
1235	AGATTAGTAAATGCTGCGCC
1236	ACTATGATAACAGCAGCCCCG
1237	ATATGAATAACTCCAGCGCC
1238	AGACTGAAATCTACAGCCCCG
1239	GTACTGATAATTGGATCGCC
1240	CCAGAACGGTTGCAGACACT
1241	GCAATAGTTGGACCCAGGCT
1242	GGAATAGGTGGACTCACTCA
1243	GCACAAGTTTCGCGCATCGA
1244	GCGGAATCTGTGCAGCATCT
1245	GCGAGAATATGGTGACATCT
1246	GCGGTCAATTAGTGGACTION
1247	CTCCTACAATGGTGACACTG
1248	CTATTACAATGGTATGCCCG
1249	AATCATACAAAGTGTGCCGC
1250	CATGATCTAAGAGTGTAGCC
1251	CAAGAAGTAAGATGCGTGCC
1252	CATGTGATAAGATGTGGACC

אנו מציינים כי המידע המוצג כאן אינו מהווה ייעוץ משפטי, ולפיכך אינו מהווה חלק מהסידור.

Seq. Id	3' to 5' sequence
1253	AACCTAGCAAACCTTAGCGCC
1254	TCTTCGATATGATAGCGTCG
1255	GACGTTAATTGATGAGACGC
1256	GCGTGAAGTTGTTAGCACAT
1257	GCCGATACATGCTGCACGAT
1258	CGCCGATTAAGCTGCGACAT
1259	CGTCATTTAAGTTAGCGCAC
1260	CTCCATCTAAGGTGCGATAC
1261	CGCTTATCAAGGTGCAGACC
1262	GATGACTCAATGTGACTCAG
1263	CGCTAGTGACAATTATGTGC
1264	GCTAGGTGACAGTATGCTAT
1265	GCTGTGCTACGACGTTGACA
1266	GCTAGAGTAGACCGATGCCA
1267	GTATATCGAGATCATAGGCG
1268	GTCTTGGAATATACGAGCGC
1269	TACTTGTAGATAGCGAGCGA
1270	GTAATCTGACATGATTCGCA
1271	TATACTGACCTTATCGGCAC
1272	TCGTCTTGAGATATGTGGAC
1273	TCATGTTACGGTATGCGAGA
1274	TCATCTGCACGTATCGTCAA
1275	GCGACTGGACAGATTGCATA
1276	CGGGCGCGAAGTATTCACAT
1277	GTGTGGGCACGTATTCCATA
1278	TCCGGGCACGGTGTCTATATA
1279	TGGGCGCTACTGGCTCTTAA
1280	TGCGCCGCCAGTCTGTTATA
1281	TGGCCGTTAGAGTCTGCACT
1282	ATGGGCGCAACCCTGTCATA
1283	CAGCCCTGAAGACTGCGATA
1284	CGCCGCTCAAGGCTATGATA
1285	CGCTCCTGAAGGGTAGTTAA
1286	GGCCCGACAGGTGCTATTAT
1287	GGATAGGCAGATGCACTTAT
1288	GGACAGACGTTGACCAGCTA
1289	GTAGCGACATTGAGTTAGCA
1290	GACTACGAATTGAGCATACG
1291	CTACACTAATTGCAGCAGCA
1292	CGTACCCGAATGCAGCAGAA
1293	GACGCCTAATGACGCTGAAA
1294	TAGCTTGTAAGTGCAGTACG
1295	GATACTCTAATGCCATCGAC
1296	CGGCGTACAATGCCATAGAA
1297	CGGATACGAAGGCTATGCAA
1298	ACGGATCGAAAGGTATAGCC
1299	ACGGCGCGAAAGCGTCATAA
1300	CGTGAGGGAATACGTCATCA

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Seq. Id	3' to 5' sequence
1301	CACAGTGAAGACGCATCAC
1302	GAGGTGACATGACGTACATC
1303	GAGTAGCGAATGCTCAGCCA
1304	TATAGCACAGTGTCCAGCAA
1305	CGTATGTCAAGGGCCTGATA
1306	CGAGACGCAAGGGATTACACA
1307	GAGACGCAATGTGAATTACG
1308	GATCGCACAGGAGCGTATCA
1309	TGCCCAGAGCGTATGAGCAA
1310	TGAGGGCGAGCTATCTATCA
1311	TTGTGGCTAGGTATCGCTAC
1312	TGGTTAGCAGGTATGATCCT
1313	CTCACTGCAAGGATGGGACT
1314	TCCTGTAGATCCCTATGCGG
1315	TCGTTGTCAGCATATTGAGC
1316	ATCATGTGAACCTATTGGCC
1317	TACACTGGGACCTATGGGCA
1318	TACCTGGGAGCATAGCTGAC
1319	TAGCCCGCAGCATAGGGTAT
1320	GAGCCTCAATGCTACGGAAG
1321	GATGTTCAATGCTGGCCGAA
1322	GACTTGTGAATATCTGTGCC
1323	GCCGCCGAATTATTGAGCAA
1324	TGGACTGATTGATAGGCAAC
1325	TGGCAGATCGGTGTATTCAA
1326	TATGCGTAATGGGTGTTCCA
1327	TTAGGTCGATTGATAGTCGC
1328	TCTGCTTTACTGCGTAGCCA
1329	TTGACGAGTTTGCAGTGCTC
1330	CTTGATTAAGTGCTGTACGC
1331	CTCGGATCAAGGCTTACCGT
1332	CCGGGCTCAACGCTTTGTAA
1333	TGTCGCCCAGCTCATGTGTT
1334	CTGGACCCACAGCTATGGAT
1335	CACGGGCCAAGAGATATACC
1336	CGCCCGCCAAGTGATGTATA
1337	CGCCAGCCACATGGATAGAT
1338	GCCCGGATACATGCGATTAG
1339	GCTGGCCTACATCCGTATGA
1340	AGATGGCGAAATCCGTATAG
1341	GCAGGGACATTACGATCAGT
1342	AGCAGGTGAAATCGTACTAC
1343	GCAGGTCAATCTCTGTACGA
1344	GCATTGTAAGTTCGGTCAAG
1345	GCACTGGTAATTCAGCTACG
1346	AGCATCATAACCCAAGCTGG
1347	ACCAGTCCAAAGCATAGTCG
1348	ATCATTTCAACGCAGTGACC

Seq. Id	3' to 5' sequence
1349	TCAGCCCTATCGCAGGATGT
1350	GTCAGCACCAGCCGTGATTA
1351	GAATTACGCACCCAGCTTGA
1352	GAATGCGCCTACCAGCTATA
1353	GAATGGCGACAGCGTACATA
1354	GGATTGCCACGACTCACAAA
1355	GCTCATTGACACTGCGCTAT
1356	GAGCATGGACCACGGCTATA
1357	CAAATGGACAGACAGCCTGC
1358	CACTTTGAAGCACAAACACG
1359	GCTGTTGCAGGACGCATCTA
1360	TACCTGGCATGACGCGATAT
1361	TTCGTGGACTTGCGGATCTA
1362	TTCTTGCGATAGCGGCGTTT
1363	TTGATCTGATAGCGGGTCTC
1364	TTGATCGCATAGCGTCTGAC
1365	TTCGAGGCATGTGGATCTCC
1366	TTCAGCGGCTAGGCGATTTC
1367	TCCAGCAGATCGGCGAGTTT
1368	TTCAGCCGATCTGCCGATAT
1369	TTCTATCGCATGTCAGCCGT
1370	TGTAATGCCTGCCAGCCGTA
1371	TAATTGCCTGCACAACTGGA
1372	TAATTCCATTGACGGCAGCG
1373	TTATTGCCATAGCGCGACGC
1374	ACAATTTCAAAGCCTGACCG
1375	ACAGGCCCAAAGCACTAGGT
1376	CGAATGCCAAGGCCAGCTAA
1377	GATGGTTCAATGCCTGGACA
1378	CTGGGCCAAGTTCTGAGACA
1379	CGTGGGCAATACAGTTGAAT
1380	GAGCTGCGAATCGGTATTAA
1381	GACCGGCGAATCGAGCATAA
1382	GACTTCGCAATCGGCACGTA
1383	GACGCGCCAATCGTGCTATA
1384	GATCGCTGAATCGTGCGTAA
1385	GATCACTGAATGCGACGTAA
1386	GATCGTGCAATGAGGTTACA
1387	GAGGACTAATTGAGATGCAC
1388	GACCGATAATTCGATATGCC
1389	TAGCATTGATCCCATGTCAC
1390	TTCAGCTTATGCCAGTCGCG
1391	TGACGGCCTTGATATCCGA
1392	GAACGCGCCTTACATCAAGA
1393	GAATACCAGTTACACTCCAG
1394	CAAGAACTGTTACACATCGC
1395	GACGAGAATGGACTACACGT
1396	TACAGACGCTTGATAGATC

Seq. Id	3' to 5' sequence
1397	TAACGACCTTAGCGACGGGT
1398	TAACGACGCTTTCCCAAGGA
1399	TTACCGCTGTTGAGCCCGTA
1400	TTCCATGTATCGAGCGTCAG
1401	TATACGCCCTTCAGATCGGG
1402	CTAAGCCTATGCAATATCGC
1403	CCAGCTATAAGCATATTGCC
1404	TACAGCATTGTCATGGACTC
1405	TAAGCTATTGGACATTGGGC
1406	TTAGCATCCTGTCATAGGGC
1407	TCTAGCAGCTTTCATAGCCA
1408	TCATCACGCTTCCGAGGAT
1409	GCATACATTGGACGAGAGCT
1410	TCTAGCATTTAGCATGGTGC
1411	TTATGACTTGATCTGAGGCG
1412	TGTTTCGCACTGGCTTAGCTC
1413	GAGTTGAATGCAGATAGCTC
1414	TGCAGGCTCGCAGATGCTAT
1415	TGCGAGGACTGTAGCTTAAT
1416	TGGGCACTCTCGCCTAGTTT
1417	TGAAGCGCCTCGACTAGGTT
1418	TCATCGGCACTGATAGCTCA
1419	TCATCAGGCATGGAGCCAGT
1420	TAATCAGCGTTACGTCCGCA
1421	GAATGTGACGCAAGTCTGAC
1422	AGATTTGCACAGATAACGCG
1423	GATTACTGACCAGCATCGAG
1424	AACTATCGAAACCGCCAGGG
1425	ATAATACAAGAGTCGCGCCG
1426	ATAATCATAACCTCGACGCG
1427	ATTATCATAAAGGCAGGCG
1428	TATATCGGATCAGCAGGTCA
1429	TAATTTTCGCTACGCAGGGAG
1430	TAATCCTGTTACGCGGAGGC
1431	CTTTAGCTCCACGCAGTGTG
1432	TTCTAGCCGTCCGCAGTTTG
1433	GTCATGCGAGCAGCAGTCTT
1434	GGCGTTCGAGCAGTCATCTT
1435	TACCGCCAGTCAGCGAGTTA
1436	TACCGCCTAGCAGCATTGGT
1437	TACCGCACTGCATGTCAGGT
1438	TGTCTCGATGCAGGTCTAGT
1439	GCCGCATGACGAGGATATAC
1440	TACCGCGAGGCAGGATTCTT
1441	TACAGCAGTGCAGGGCCTTA
1442	GCAGCTAGAGCAGAGTATCA
1443	GACAGCAGATCAGAGACTCC
1444	TAAGCACGTTTAGAGCTGAC

Seq. Id	3' to 5' sequence
1445	TAACCGTGTGCAGATCGGAT
1446	TACTGCGGACCTGGATCTAC
1447	TCAGGGCTACTCGATTGGAA
1448	TCCGCAGACTTAGCGTTACG
1449	TGAGCAGCCTACGTTACTAG
1450	TGCGTCAGATGCGTATATGC
1451	TCGTCCAGATGCGGAGTTCA
1452	TCGGCTATATGCCAGATCCT
1453	AAGGACAAAGAGCGCGTCTC
1454	TAGCACCGATGGCGAGCTTA
1455	TGTCCACGGTGCCGCAATAT
1456	TGGTCCGACTGCTGCTACTA
1457	TGTGCCGACTGCCGTCTTAT
1458	TTCGCAGTATGGATCGGTAT
1459	TTACGCAGTTGCATGGAGCT
1460	TTCTGATTAGCTGCGGACGC
1461	TGGTTATACTTTGCGAGAGC
1462	TTTGTTAGCTTCGGGCAGCC
1463	TTGGTCTGATCCGGGCATAC
1464	TGCTTGGACTCCGGCGATTA
1465	CTGCTTGGACCAGCCAGTTA
1466	AAGCTGGGAAACGCACACCT
1467	AAGCGGGCAAACGATATGCT
1468	AAATGCCGAAACCATCTCGT
1469	CCATTCCGAAGCGACTCGAT
1470	TACATGGGCTGAGAACGCAA
1471	TATTGGGCACGAGCGCCTAT
1472	CATCCGGGAAGAGTAGCACA
1473	ATTTTCATGCACATAGCACGC
1474	ATTGCAGCACAAGCCAGACT
1475	TTGCTAGGCTCAGTCCCGAT
1476	TTGGCGAGCTGCGTTCTCAT
1477	TCCCAGAGATGCGACTGCTA
1478	ITCGCTGGATCGGCATGTCT
1479	TTGCTCCTAGCTCGCGTGAT
1480	TTGCTGCTAGTCCAGTAGGC
1481	CATTAAGCAGTCGAGAGACC
1482	CGTTAATGCAGCGAGAATCA
1483	CGCAAGCTCAGCAGAATTAC
1484	CCATGTCTGAAGCATTATAC
1485	CTGAATGTAATCATCGTGCC
1486	CTTAGATGAATCACTGCCAC
1487	CTTCACGGAATCTAGGCACA
1488	CACCTTTGAAGCTAAGCACA
1489	CCTCTAAGCATGTTGACACA
1490	CATGCCGGAAGATGCGTACA
1491	CAGGCAGCAAGATGTACGAC
1492	CAGTGGGCAAGATAAGATTG

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Seq. Id	3' to 5' sequence
1493	CCGTGCCCAAGCTAGTGATA
1494	GATCGGGCAATCTGCGTACT
1495	TTCAAGTGCATTATAGTGCGG
1496	TTATCTGCATGAGTAGGTCG
1497	TCGATAATCTTTGTAGCGCG
1498	TCTTACAGCTTTGCAGGGAG
1499	TCCTACATTTGCCACGGGAG
1500	TCTTCATCAGTGAGGCGCGA
1501	TTTCTAGGATGTATGCGAGC
1502	TATCCAGCATTACTGCGAGA
1503	TTATTCTCAGCACGCACGGA
1504	TGATTGCGACTCGCGGCTAA
1505	TTTGTATGAGTCGCTCCGAA
1506	TTCCGATCAGTCGATGCAAA
1507	GATCGTCAATCTGATGCACC
1508	AGATCGCTAAATGAGGACCC
1509	GATGCTATAATCGTATGGCC
1510	AGGAGCGTAAATTATCAGCC
1511	GGGCGATGACTATATCTGAA
1512	CTGGATTGACACTAGCATAC
1513	CTGCGGATACCATAGACAAC
1514	ACTGCAATAACATATCCGCG
1515	AATGACATAAAGTGCTGCCC
1516	ACATGCAGAAAGTAGTCCGC
1517	ACAGGCGAACAATGTACCCG
1518	ACCAGCACAAAGTCTACTGT
1519	AGAGAGCCAAATGACTGTCC
1520	TAGTGCATAATTGCTTGCCC
1521	TGAGCATATAGTATTGCGGC
1522	TGAGCGTTAGAGCTTGATCC
1523	TAGGCGCTAGGACTCGTTAT
1524	TATGGCCGACGATGTGTCAC
1525	TATGGCTGACGTAGCGCACT
1526	TCTCGGTTACTGAGTGGAAT
1527	ATAACGGGACAGAAGCTGCT
1528	ATAGAACTCAATAGCCGCTC
1529	CATAATACACATACGCTGCG
1530	CAGTACGCAAGCAGATAGCC
1531	CAGACGCGAAGATAAGTTCC
1532	CAGCCAAGATAGCATACTCG
1533	TCCCATAGATAGCTCGCTGG
1534	TTCGCATGAGTGCTGAGTAC
1535	TTCCATATACTGGTCGGCAG
1536	TTTATGATATGCGTCGCGGA
1537	TTTCTTATATGCGCGAGCGG
1538	TGTTGCATATTAGCGGCTCG
1539	TATATGACATCTCTTGCCCG
1540	TTGTACATTTGCGCTCCGA

Attorney Docket No. 3108.1

Seq. Id	3' to 5' sequence
1541	GCATCCGAATTGCGACGACT
1542	GGATCTGAATTGCGCGACCA
1543	GGCTATGAATTTTCGCATCAC
1544	GGATATGCAATTTGTAGCCC
1545	CAGCGTATAGCAAGATGGAT
1546	CGAGCGATAATCAAGTCGAG
1547	CGCGGATGACACATACTCAG
1548	CGACGAGCACCAATTCGAGA
1549	CCGTAGTGACCAATGCAGAC
1550	GCGATATACATCATTCCGAC
1551	GACAGTCTAATCACTCGTAC
1552	GCAGTTATACTAAGGTGTGC
1553	GCAGTAGTAATGAGTGTCAC
1554	GCAATGTAGTCGAAGTGCT
1555	GCATATAGATACCATTGCGG
1556	CGAATACTAGACACATTGCG
1557	CAACTACAGTACACAGCGTG
1558	AGACACAGAACTACCGCGTG
1559	ATAGCACAACGTAGACGCCG
1560	ATACAGTCAACTACATCGCG
1561	AGTACAACCTAGAATCCGGC
1562	GAAGACTACTAGATACGCGC
1563	CGATAATACTACAGACTCCG
1564	CCGTGCGTACACATAGATCA
1565	CGTGAGCGACACATGATCCT
1566	CTGTAGTGACATATAGAGCG
1567	ATGTCGTCACACAGAATACG
1568	ATGCTACGAACTACCAATCG
1569	ATGATAACGTACACACCTGC
1570	TCGGTCTACGTCTGCTCAGT
1571	GGCTCACGATCCACTGGTTA
1572	TGCCTGATACCTTGGATGAC
1573	GGCCGTGAATTATCATAGAC
1574	GGCTTGGACGCATTGATAAC
1575	CCCATCGAAGCATGTGTAAA
1576	CGGCATCGAAGGCGTTCATA
1577	GCCAGTTGACCACTTCTGAG
1578	TCGCATTAGCCATGTGGAGC
1579	GCAATCTAGTCTAATGGCGC
1580	CTAAGATGTTCTAATCGCCC
1581	CCAATAGTAAGTAATGGGCC
1582	TCATTATACTCTGATGGCCC
1583	ATGCTAATAACTGATCGCCC
1584	AGTGTCAACCATGATGAACC
1585	AGAGCATAACATCATGGCCC
1586	AGAATCTAACAGCGATGCCG
1587	ATTTAGACAAGTCGATGGCC
1588	ATATTAAGAAGTAGGCGGCC

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Seq. Id	3' to 5' sequence
1685	GCATCTGTACGATCTCAGCA
1686	GCATCACGACGATTATCAGA
1687	GCTACGTTACCATGTGCAGA
1688	GCGTAGTTACCATGCTCACA
1689	GCGTGAGCACACTCTATCAG
1690	GCGTGCGAATTATGTATCAG
1691	TGTGGACACTTCTTATAGGC
1692	GCGTGAGTAATTTGACTACG
1693	AGGTGCGTACAAATGCTATG
1694	CGCAGCCGAAGTACGCTATA
1695	CGACTGCTAAGGAGCGTACA
1696	CGATGTTGACAGACCGCACT
1697	CATGTAGAACTGACTCACAC
1698	CGAGCGGTAAGGATCTCACA
1699	ACACGCTGAAAGAGTACGCC
1700	GATCTGACAGGTAGCGATAC
1701	TCTCGTGCAGGTAGCTGTCA
1702	GCTCGGACAGATCGGTATCA
1703	GCCGGTATAGCTCGATATGC
1704	GCTGATACAGTTCGATAGAC
1705	CCTGACTAAGCTCGATAGAG
1706	GCTGATTACGATCTAGTAGC
1707	GAATGCTCACGACGAGTAGC
1708	GAAGTGTCTGACGAATGAG
1709	TTACTGTCTATGCGATCCGA
1710	GTTATGTCATCGCAGATTCC
1711	AGCTATATCAAGCAAGCGTC
1712	GCTTATACAGTGCAGTAGAG
1713	TTAAGTAGGTAGCTGGCCTC
1714	CAAGAGTAACTGCAAGGCC
1715	CACTAAGACATGCACAGCGG
1716	CCTAGTGCAGACCACATGAT
1717	TCATGCACGTCGCCATAGGT
1718	TCTATACGCTCGTGCAAGGA
1719	TCAAGCCCGAGCCGAGTTTA
1720	TCAGCGCCAGCATTATGGT
1721	CCATGCGGACCAAGTCGATA
1722	GAATGCCGAGCAATGATCCT
1723	GAATCGGCAGCAATACTGTC
1724	GAAGCCCAGCTAAGTGGTAT
1725	AACAGCCCAAACCGGATGGT
1726	TAAGCACCTTGCAGGATAGA
1727	TCAGCCCGATCCAGGGTATT
1728	TATGCGCCCAGGAGGCTTTA
1729	TGCCCAGCAGGTCGGATTAT
1730	TAGCTCGCATCACTGACGGA
1731	GGTCCCATACGAGTGGCATA
1732	ACTAACCCTAACAGCGGAGGT

1733 CAGCTCTAAGCAGCACAGGA
 1734 CAGGTCAAGCACATACCAGT
 1735 CTGTGCAATCACGCCAGAGA
 1736 CGGCGCAATAATGTCACAGA
 1737 CGGGACATAATTGACACAGT
 1738 AGGGCCAGACAATACACCGT
 1739 GAGGTCACAATTTGCTACAC
 1740 CAGGCACAAGATTGAGCACG
 1741 ACAAGCGCAAATACTGCCGG
 1742 ACAATCTGAAATAGCGCGGC
 1743 ATCGACCCAAGAATAGCTCG
 1744 ATAAGCACAAGCAGCGCGGT
 1745 AACACTCCAAACCGAGGGTG
 1746 AATCTATCAAAGCGACGGCC
 1747 ATTCCCATAACGCGGAGGAC
 1748 ATGCCAGCAACGCGCTAGAA
 1749 ATGCTCACAAGCCACGAGAG
 1750 ATGCTCCAACGATACATACG
 1751 CAGCTTCAAGAGTACATACG
 1752 CATGTCACAAGGGCATAGAC
 1753 CATGGTCTAAGCCCTACAGA
 1754 ACATGGCGAAAGCACCACGT
 1755 CTTAGTTCAATGCACGCACG
 1756 CGCCAGTTAATGCACGACAG
 1757 CAGCAGCAACTCGACTAGAG
 1758 CCGAAGTCAACTGCGCTAGA
 1759 CCAGTGTCATAAGAGACGT
 1760 CCAGGCGAACTGATCGTAAA
 1761 CCTGGTACAATCAGTAGCAA
 1762 CTAGTGGCAATCATCAGACA
 1763 CAATGCGAACTCACTAGACG
 1764 CATGGCGTACCAATACCTAG
 1765 AAGTGGCCCAAATAACTGCC
 1766 CAAGGCCCAATACACAGGGT
 1767 GATCTGCCAATGCCGCGATA
 1768 GATTCGCCAATGTGCGCTAA
 1769 GAGCCGCCAATGTCACTAGA
 1770 GCGCCCGGAATGTCGTATAT
 1771 GCCGCGCCAATGTTACGTTA
 1772 CTTGCGCCAATGCGTAGGAA
 1773 TTCCCATGATCGCTGACGAG
 1774 TTGCGGGAGCTGCCTCTTAA
 1775 TTTCCCGGATAGCCGCTGTA
 1776 TTTGCTGGAGTATGCGCTCA
 1777 TTGTTCTCAGCTTGCGGCAG
 1778 TGTGTGGCAGCTTAGTTCAC
 1779 TCTTGGGTAGCATCTGTCAC
 1780 TGGGTGTCAGCATCTACGCA

Seq. Id	3' to 5' sequence
1733	CAGCTCTAAGCAGCACAGGA
1734	CAGGTCAAGCACATACCAGT
1735	CTGTGCAATCACGCCAGAGA
1736	CGGCGCAATAATGTCACAGA
1737	CGGGACATAATTGACACAGT
1738	AGGGCCAGACAATACACCGT
1739	GAGGTCACAATTTGCTACAC
1740	CAGGCACAAGATTGAGCACG
1741	ACAAGCGCAAATACTGCCGG
1742	ACAATCTGAAATAGCGCGGC
1743	ATCGACCCAAGAATAGCTCG
1744	ATAAGCACAAGCAGCGCGGT
1745	AACACTCCAAACCGAGGGTG
1746	AATCTATCAAAGCGACGGCC
1747	ATTCCCATAACGCGGAGGAC
1748	ATGCCAGCAACGCGCTAGAA
1749	ATGCTCACAAGCCACGAGAG
1750	ATGCTCCAACGATACATACG
1751	CAGCTTCAAGAGTACATACG
1752	CATGTCACAAGGGCATAGAC
1753	CATGGTCTAAGCCCTACAGA
1754	ACATGGCGAAAGCACCACGT
1755	CTTAGTTCAATGCACGCACG
1756	CGCCAGTTAATGCACGACAG
1757	CAGCAGCAACTCGACTAGAG
1758	CCGAAGTCAACTGCGCTAGA
1759	CCAGTGTCATAAGAGACGT
1760	CCAGGCGAACTGATCGTAAA
1761	CCTGGTACAATCAGTAGCAA
1762	CTAGTGGCAATCATCAGACA
1763	CAATGCGAACTCACTAGACG
1764	CATGGCGTACCAATACCTAG
1765	AAGTGGCCCAAATAACTGCC
1766	CAAGGCCCAATACACAGGGT
1767	GATCTGCCAATGCCGCGATA
1768	GATTCGCCAATGTGCGCTAA
1769	GAGCCGCCAATGTCACTAGA
1770	GCGCCCGGAATGTCGTATAT
1771	GCCGCGCCAATGTTACGTTA
1772	CTTCGCGCAATGCGTAGGAA
1773	TTCCCATGATCGCTGACGAG
1774	TTGCGGGAGCTGCCTCTTAA
1775	TTTCCCGGATAGCCGCTGTA
1776	TTTGCTGGAGTATGCGCTCA
1777	TTGTTCTCAGCTTGCGGCAG
1778	TGTGTGGCAGCTTAGTTCAC
1779	TCTTGGGTAGCATCTGTCAC
1780	TGGGTGTCAGCATCTACGCA

1781 TTGTGGCAGGTATGCTCCAA
 1782 GTTGGGCACGGATCTCTATA
 1783 GCCGAGGCACCATGCTTATA
 1784 CGCTTGGGACAATCGCGTAT
 1785 CCGCAGGGAACCTTCAGCATA
 1786 TGGAGGGCAGTCTCTCATAA
 1787 CTGGGTGCAAGTTGTATCAA
 1788 TGGCGCACATGGTGTCTATAA
 1789 TGGCATCACTGCTGCGGAAT
 1790 TGCCAGTCATCCTAGCGTGT
 1791 TCAGGCCAGGACTGCTTATC
 1792 TTGGCATAGGAGTGCTTCTA
 1793 TTTGCAGACGGTGTGCTATA
 1794 TTGAGTCAGGGTGCCCAACT
 1795 TTTAATATCGTTGCCCGAGC
 1796 TCAGGATGATGAGCATGTAC
 1797 CTCAAGCTGGGAGAACAGTA
 1798 TCAGAAGTGGCTGGATCATA
 1799 TCTCACATGGCTGGAGCATT
 1800 CTAAGTACACTGACCAGGGA
 1801 TCGTAGCGACTCTCCAGGTT
 1802 TACGTGTCACTATCGTCGAG
 1803 TATAGTTACGTCTCGCACGC
 1804 TACCGTTACGTGCTCAGAG
 1805 CACTACAACGTGCTACAGAG
 1806 ATAGGTATAACGCAGTACGC
 1807 ATAGCAGTAACGCATAGTCC
 1808 ATAATCGTAACGCACCGACG
 1809 ATGAGTGTAACGCCTCGACA
 1810 ATGTAGCGAACGTAATCACA
 1811 ATCTAGCGAACGGAATATC
 1812 GTAGAGTCACGATGCAGTAC
 1813 GTAGTATGACGTAGCAGTAC
 1814 GTACGTCGAGCTAGATCGCT
 1815 GAGTCTGTACGAGGTATCAT
 1816 CGTGTCTTACAGCACTACAT
 1817 CGTGCGCTACAGCAGTCATT
 1818 GTAGCCTAGACGCAGTCGTA
 1819 CGTCTCGCAAGTCGCGTATA
 1820 AGTCGCGCACAGCAACGTAT
 1821 ATCGAGGTAAACGCCATATAC
 1822 CTCGTGACATAGCCATAGAT
 1823 ATGCGACGAACGCGGATATA
 1824 CTAGACAGACTGCGACATAC
 1825 TAGTCGTAGAGGCGCTATCA
 1826 CTATCGAAGTCGCGTGAAAC
 1827 CTGCGTATAGAGATCAATCC
 1828 CCGCGTATAGACAGATATGA

Seq. Id	3' to 5' sequence
1781	TTGTGGCAGGTATGCTCCAA
1782	GTTGGGCACGGATCTCTATA
1783	GCCGAGGCACCATGCTTATA
1784	CGCTTGGGACAATCGCGTAT
1785	CCGCAGGGAACCTTCAGCATA
1786	TGGAGGGCAGTCTCTCATAA
1787	CTGGGTGCAAGTTGTATCAA
1788	TGGCGCACATGGTGTCTATAA
1789	TGGCATCACTGCTGCGGAAT
1790	TGCCAGTCATCCTAGCGTGT
1791	TCAGGCCAGGACTGCTTATC
1792	TTGGCATAGGAGTGCTTCTA
1793	TTTGCAGACGGTGTGCTATA
1794	TTGAGTCAGGGTGCCCAACT
1795	TTTAATATCGTTGCCCGAGC
1796	TCAGGATGATGAGCATGTAC
1797	CTCAAGCTGGGAGAACAGTA
1798	TCAGAAGTGGCTGGATCATA
1799	TCTCACATGGCTGGAGCATT
1800	CTAAGTACACTGACCAGGGA
1801	TCGTAGCGACTCTCCAGGTT
1802	TACGTGTCACTATCGTCGAG
1803	TATAGTTACGTCTCGCACGC
1804	TACCGTTACGTGCTCAGAG
1805	CACTACAACGTGCTACAGAG
1806	ATAGGTATAACGCAGTACGC
1807	ATAGCAGTAACGCATAGTCC
1808	ATAATCGTAACGCACCGACG
1809	ATGAGTGTAACGCCTCGACA
1810	ATGTAGCGAACGTAATCACA
1811	ATCTAGCGAACGGAATATC
1812	GTAGAGTCACGATGCAGTAC
1813	GTAGTATGACGTAGCAGTAC
1814	GTACGTCGAGCTAGATCGCT
1815	GAGTCTGTACGAGGTATCAT
1816	CGTGTCTTACAGCACTACAT
1817	CGTGCGCTACAGCAGTCATT
1818	GTAGCCTAGACGCAGTCGTA
1819	CGTCTCGCAAGTCGCGTATA
1820	AGTCGCGCACAGCAACGTAT
1821	ATCGAGGTAAACGCCATATAC
1822	CTCGTGACATAGCCATAGAT
1823	ATGCGACGAACGCGGATATA
1824	CTAGACAGACTGCGACATAC
1825	TAGTCGTAGAGGCGCTATCA
1826	CTATCGAAGTCGCGTGAAAC
1827	CTGCGTATAGAGATCAATCC
1828	CCGCGTATAGACAGATATGA

1829 1830 1831 1832 1833 1834 1835 1836 1837 1838 1839 1840 1841 1842 1843 1844 1845 1846 1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864 1865 1866 1867 1868 1869 1870 1871 1872 1873 1874 1875 1876

Seq. Id	3' to 5' sequence
1829	CTCGCTTACGACAGACTGGA
1830	CGCGCACGAGACATAGCTTA
1831	AGCGTCACACACAAGACTGG
1832	CCTACGAGACACATGACAGG
1833	CGCCGAGTACACATGCAGAT
1834	CCGTCGATACAGACTCAGAT
1835	CTCGTCAGACAGAGCGGATT
1836	GTCTCGCCACGTATCGGATT
1837	TCTCGCGTACTTAGGCATCA
1838	GTCTCGGTACGATGTAGCAA
1839	CGTGTGAGACAGTAGCATAT
1840	CGTGTAGCACAGCGACGATT
1841	GTGTAGCTCAGTCAGCATCA
1842	AGGTAGATAACGCTAGATCC
1843	CTGTAGAGACATCTGAATCC
1844	CTGATACGAAGTCTTATGCC
1845	CACGCTCGAAGACTAATGAC
1846	CACGCGATAAGACGTATAGC
1847	CTAGCAGTAAGTCTATGCAC
1848	CGTAGTTGAAGTCATCGACA
1849	CGCGATAGAAGTCAGGACAT
1850	GACGGACGACATCTGAGCAT
1851	CATAGACGAATACAGCGGGC
1852	GATCACGACCTACTAGCAGG
1853	AGATATAACGAACTCTCGCG
1854	GATTATAGACTACTGAGGCC
1855	GAGTTTATACTACAGTGCCG
1856	GTCAC TTACGCTCAGGCAGA
1857	TCGCTAGACGCTCTGGCATA
1858	GTACGCTCAGCACTGGCATT
1859	GACGCGCTAATACTGTCACA
1860	GCGTGCATACGACTGCCATA
1861	TGTAGTCTAGTGCATGGTCA
1862	GTATAGTCAGAGCTGGCACC
1863	CGTCAGTCAAGTATGGCACA
1864	ACGAGAGTAAATATGCTGCC
1865	ATAGAGCGAACGATAGTTGC
1866	ATCTGACTAACGATGATGCC
1867	GTTGTAGGACGTATGATCTC
1868	TTAGTCGAGTCTATGAGCCC
1869	CGACGATACAGTAATCTAGC
1870	CTGATACAGGCATAGACATC
1871	GGTATCAGAGCTAGGACTAT
1872	TCTATCTCAGCTACGGTCGA
1873	TCAGTTCGATCTACGGCTAG
1874	TCAGTGCGACTCAGGTACGA
1875	GTCAGTGCCTCACGGTAGA
1876	TAACGAGTCTTCAGCACGTA

1877 GAAGTCGCCTACATAGCCTA
 1878 GAAGTCCGTTACATGACCAT
 1879 GTCAGAGGATCGAGCCACTT
 1880 GCGAGACAGGTCAGTACAAT
 1881 CGTCAGAAGGCTCGCACATA
 1882 GCATACAGGTTACGACGCCT
 1883 GCGATACAGGTTACAGAGATA
 1884 GGACGCATAGCTCGCAGTAT
 1885 GGACGCAGATCGCAGCATAT
 1886 CGGCGTTAATCGCAGAGAAC
 1887 CGCGTTCTAAGGCACGGATA
 1888 CGCGTCGCAAGGCTGTTATA
 1889 CGATACGCAAGGCTACGACA
 1890 CATCTAAGGACACTACACTG
 1891 TATCATCGAGGACTCAGTGC
 1892 CACCGAGCAAGACTGACATG
 1893 CGCACCCGAAGTCAGAGATA
 1894 CGGCTAGGAAGTCAGCATAA
 1895 ATGCTGCGAACGCGCCATAA
 1896 CCGCGTGCAACGTGTTTATA
 1897 GTCGCTGCATAGCATCTCAG
 1898 GTCTGTGCATAGAGCGTCAT
 1899 GTGGTGCTACTGATACGTCA
 1900 GGTTAGCACTAGATCGCACT
 1901 CGGGATCTACAGCATCATAG
 1902 CTGGATATACAGCACTCACA
 1903 ATGCGGCTAACGCCTCATAA
 1904 TCGCGGCGCACTCTGTTATA
 1905 TCGTGCTACTGCCACTGTAT
 1906 TAGGACACTTCGCCACTATG
 1907 TATGACAGTTGCGGCTACCG
 1908 TCGCGCAGTTAGCCCTATGT
 1909 TAGCCACCGTAGCTGATCGT
 1910 GTAACCCGCTATCAGATCGA
 1911 AGAGCGCAACACCACATTGT
 1912 AGGCTAAGAACGCACACTCG
 1913 GAGCCTAGACAGCTTCATAC
 1914 GGCAGTTCACGACTCGACAT
 1915 GGCCTTAGACGACTCGCATA
 1916 GGTCGATCAGCACTGCATAC
 1917 GGAGAGTCAGCACAGTCCTA
 1918 GTATAGGCAGCACGGCTCAT
 1919 GCACGGCGAGCACTATCTTA
 1920 TAACGTCCTGCACGATCTGT
 1921 GGACGCCTAGCACATCTGAT
 1922 CGCTGCACATCACATGGATT
 1923 GCACATCGAGCACATGCAGT
 1924 GCACGACCAGCTCTTAGGAT

Seq. Id	3' to 5' sequence
1877	GAAGTCGCCTACATAGCCTA
1878	GAAGTCCGTTACATGACCAT
1879	GTCAGAGGATCGAGCCACTT
1880	GCGAGACAGGTCAGTACAAT
1881	CGTCAGAAGGCTCGCACATA
1882	GCATACAGGTTACGACGCCT
1883	GCGATACAGGTTACAGAGATA
1884	GGACGCATAGCTCGCAGTAT
1885	GGACGCAGATCGCAGCATAT
1886	CGGCGTTAATCGCAGAGAAC
1887	CGCGTTCTAAGGCACGGATA
1888	CGCGTCGCAAGGCTGTTATA
1889	CGATACGCAAGGCTACGACA
1890	CATCTAAGGACACTACACTG
1891	TATCATCGAGGACTCAGTGC
1892	CACCGAGCAAGACTGACATG
1893	CGCACCCGAAGTCAGAGATA
1894	CGGCTAGGAAGTCAGCATAA
1895	ATGCTGCGAACGCGCCATAA
1896	CCGCGTGCAACGTGTTTATA
1897	GTCGCTGCATAGCATCTCAG
1898	GTCTGTGCATAGAGCGTCAT
1899	GTGGTGCTACTGATACGTCA
1900	GGTTAGCACTAGATCGCACT
1901	CGGGATCTACAGCATCATAG
1902	CTGGATATACAGCACTCACA
1903	ATGCGGCTAACGCCTCATAA
1904	TCGCGGCGCACTCTGTTATA
1905	TCGTGCTACTGCCACTGTAT
1906	TAGGACACTTCGCCACTATG
1907	TATGACAGTTGCGGCTACCG
1908	TCGCGCAGTTAGCCCTATGT
1909	TAGCCACCGTAGCTGATCGT
1910	GTAACCCGCTATCAGATCGA
1911	AGAGCGCAACACCACATTGT
1912	AGGCTAAGAACGCACACTCG
1913	GAGCCTAGACAGCTTCATAC
1914	GGCAGTTCACGACTCGACAT
1915	GGCCTTAGACGACTCGCATA
1916	GGTCGATCAGCACTGCATAC
1917	GGAGAGTCAGCACAGTCCTA
1918	GTATAGGCAGCACGGCTCAT
1919	GCACGGCGAGCACTATCTTA
1920	TAACGTCCTGCACGATCTGT
1921	GGACGCCTAGCACATCTGAT
1922	CGCTGCACATCACATGGATT
1923	GCACATCGAGCACATGCAGT
1924	GCACGACCAGCTCTTAGGAT

Seq. Id	3' to 5' sequence
1925	CCCACCAGACAGATAGAGGT
1926	CCCGACGCACGAATAGATAG
1927	CCCACGACAGATACATGAGT
1928	CTTCGCGCAGCTACATAGAT
1929	CGCTCCGAAGCTGCGATAAT
1930	CGCCGCGTAAGCAACAAATT
1931	CGACGCTCAAGGACTCATAA
1932	CGCACACTAAGGATCATTAC
1933	AGACACGCAAGAAGCTGGCT
1934	GCACGCATAGCAGAGGATCT
1935	GCTACGTCAC TGAGCAGGAT
1936	GTACATCTCGTGAGCAGAGC
1937	CTACACGACTTGAGACGAAG
1938	CTAAGTACGTGCAAGCAAGG
1939	GACACGTAGGACAGCTATGC
1940	GACATAGTAGACATCTCACG
1941	GACAGCGTAGACATCGTCAG
1942	GACTATCACGACATTCAGCG
1943	GATCTACACGCTACCAGTGG
1944	GCTTACTACGGATAGATCAG
1945	GCGTATCTAATGGAGTAGCA
1946	GCGTATTTACAGTGAGCGAC
1947	GCGTATATCGAATTGAGTGC
1948	GCGTTCACAGAGTCCACGAT
1949	CGCGTATCAAGGTCACGACA
1950	GCTATTACAGTGTCAGAGAC
1951	CGTCAGATAAGGTGAGTTAC
1952	CGTCTGTGAAGGTCAGCTAA
1953	TATTAGCACTCGTCAGCAGC
1954	ATGTTATCAACGTCAGCGAC
1955	GGCATACTAGAGTCAGCGAT
1956	AGTGCGATACAATACGAGCG
1957	CAGCACACAGAGTACAGCGT
1958	CGTAGCATAAGGTCAGCACC
1959	GTCCATAGACGTTGATACCA
1960	GCTACGATAGATGAGCCACG
1961	CGGAGTACACCAGATCCAAG
1962	GAGCGTATAGGAGATCCAAC
1963	GACTGTAGAGAGACGATCCA
1964	CTAGTAGGAAGTGCGATCAA
1965	CGTAGAGGAAGTGATACTCA
1966	CGTATCGGAAGTGAGTATCA
1967	CTATGACGAAGTGAGAGTAC
1968	GTTTCGTAGAGATGATCGTCA
1969	GTTCTCAGATAGTATGCAGC
1970	AGTCTGTAAAGATATGCGCC
1971	AGCACGGAACAGTAAGCCCT
1972	ATCCAGAGAACGTGAGATCC

Seq. Id	3' to 5' sequence
1973	GACAGTGTAAATATGAGGACC
1974	CATAGTAGAAGATTTCGAGCC
1975	TGAGATATAGTATGCGGCCA
1976	ATGAACATACTATAACCGCGC
1977	TTCTCTATATCGTGCGCGGA
1978	TGAGTTTACGTGTATGGCAC
1979	ACGGCATCAAAGTTGCATAC
1980	ACGGGCTCAAAGTATGATAG
1981	AGGCGCTTAAATGTGGATAC
1982	CTGCCGTTAATGGCGGACAT
1983	CTGAGCCAATAGGCGCACTT
1984	TAGGCATGATGAGAGCTATC
1985	TGCCTATGAGGAGTATGAAC
1986	GGGCTATAATGAGCTTGAAT
1987	TAGGCTTCATCAGCTATCAG
1988	ATTGCTTCAACGGGCATTAC
1989	TATGATCCATGCGACTCGGA
1990	TTGTATCCATCGGCCAGTG
1991	ATCAAGGCAACCGCCAGTAG
1992	TCTCAGCCATCCGTGATAGG
1993	TATCAGGCATCCGAGCATAG
1994	TTAAGCTCCTCAGTCCATGT
1995	TAAGGGCGATGAGCCTATCT
1996	TAAGGCCGAGGAGCTTTCAT
1997	TAAGGCAGTGGAGCCCTCTA
1998	TGGACAGGCTGCGCTCTATA
1999	CTGGAAGCCTGCGACCAAAT
2000	TCAATGCACTGAGCCCGAGA
2001	GATTCACACTGACCCATGTA
2002	TAAATAGATTGGAGACGCGC
2003	GCATTAGAAGGTCTGGACTA
2004	ATTGGCATAACGTATTGCGC
2005	CAGGACTGAAGATCGAGTAC
2006	TAGAGTCAGTCATAGCTCGA
2007	TTTATCGTAGCTGGCTGCCC
2008	AGGATTAGAACCTACGCACC
2009	GCCGTGAGACCACTGTACTA
2010	GACGCTGAATCCTATTGACA
2011	CGCCTAAGGATCGTGAAGTA
2012	CGACGACGAAGCTGCATGAA
2013	ACTCGAATAACAGCATCTCG
2014	CCCGTAAGCATGGCACAGAT
2015	CAATACAAGATTACGGCCTC
2016	GATCAGAATCTATGGTACGC
2017	TCTGTGTACTGCTCGCCAAT
2018	ATATTTGGAACGCAGCTCAC
2019	TGCAGTATCGCAGCGGTTCTA
2020	GGGCAATGTTTATCCACAGA
2021	CTGACCGAATCCAGCAGAGA

Seq. Id	3' to 5' sequence
2022	GATCGTGAATCCGCGCACTA
2023	GAGCCGTAATCCGAGCGATA
2024	TACTCCTGACGACTTAGGCA
2025	TGCTGTCACTCGGCGTCTAT
2026	GTACTAGCATATCATCGACG
2027	TATCGCATAGATCAGTGAGC
2028	TACGGGCAGCCAGGTACTTT
2029	GTTTCATCACGAGTGCGTAGA
2030	CATGTATCAAGATGGCTGAC
2031	GGTCGCGCATTCCAGCATA
2032	GCACATATCTAGCGACATCT
2033	ACGCGGCTAAAGGTAGATAC
2034	CACTGCCACAAGATGTAGA
2035	GGATTTACATGGCCTAGCAA
2036	CATGACACAGAATCGACCGT
2037	AGAGGCATAAATGAGTCTCC
2038	TGAGTAGTACGTTACGCCTG
2039	CGATAGCGAAGGAGTCCACA
2040	ACACTCTGAAAGACGCGACG
2041	GTCTTAATGTTGGGCAACG
2042	GTTATCGACTACGCTGTACT
2043	TCGTGAGACCGTCGTCAGTA
2044	GACAGCGCAGTACAGGTAAT
2045	CGTACAGTAAGTATGATGCC
2046	TAGAGCATCTGACGCTATGA
2047	GTCACGATTAGTAGGCACG
2048	TCGTACCTGTATTACGCGCG
2049	TTAATCCGCTGTAGCCCAA
2050	TTAATTGACTTCGCTCCAGC

EXPERIMENTS

Arrays containing probes corresponding to SEQ ID NOS 1-2050 were designed and manufactured using known photolithography techniques. Four probes were designed to interrogate each sequence from SEQ ID NOS 1-2050: a probe designed to be the perfect match complement to the sequence (PM), a probe designed to have a central mismatch at position 10 (MM), and probes designed to be the complements to the PM and MM probes (cPM and cMM respectively).

FIG. 2 shows an example of the sequences attached to each of the four array features representing a given tag sequence. The first block contains the cPM probe. The second block contains the cMM probe. The third block contains the PM probe - the probe to which the tag is expected to hybridize with the highest affinity. The fourth block contains the MM probe.

FIG. 3 shows the array features from the above-described array. The array was hybridized with biotin-labeled oligonucleotide tags, stained with streptavidin-phycoerythrin, and the data was collected with a laser scanner. Four features, organized vertically on the probe array, represent each tag-probe. For each of the four tag-probes shown, arranged horizontally across the array, the brightest hybridization signal is seen with the “PM” feature.

FIG. 4 is a scanned image of the hybridization pattern resulting from the hybridization of 2050 different oligonucleotide tags labeled with phycoerythrin to an array designed as described above.

FIG. 5 is a scanned image of the hybridization pattern resulting from the hybridization of 50 sequences complementary to SEQ ID Nos. 2001-2050 to an array designed as described above.

FIG. 6 shows signal intensities from two different independent experiments in which 2000 biotinylated oligonucleotide tags or 50 fluorescein labeled control oligonucleotides were hybridized to arrays designed as described above. The frequency of results are shown as normalized (to scale of 0-1, in bins of 0.05) natural logarithms of the net signal intensities. The normalized natural logarithm of the signal intensities obtained are distributed about a geometric mean of 0.8 with a standard deviation of less than 0.1.

FIG. 7 shows the PM/MM ratios from the data described in FIG. 4 above. More than 98% of the hybridization's yielded a PM/MM ratio greater than 3/1.

CONCLUSION

The above descriptions are illustrative and not restrictive. Many variations of the invention will become apparent to those of skill in the art upon review of this disclosure. The scope of the invention should, therefore, be determined not with reference to the above description, but instead should be determined with reference to the appended claims along with their full scope of equivalents.

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